

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 4, 2003, 10:26:31 ; Search time 1926 Seconds
(without alignments)
9044.356 Million cell updates/sec

Title: US-09-898-556a-3
Perfect score: 2772
Sequence: 1 cagcgcggttaagctggttg.....ttctaccatctcaccct 2772

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 7090273 seqs, 3142032823 residues

Total number of hits satisfying chosen parameters: 7894758

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database :

Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/1/pna/PCN_NEW_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq2:*
7: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq3:*
8: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2:*
10: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*
11: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33.6	1.2	51	5	US-09-749-280B-127
2	33	1.2	41	11	US-60-449-155-509
3	31.6	1.1	51	5	US-09-749-280B-128
4	27.8	1.0	55	6	US-09-912-293-242606
5	27	1.0	60	1	PCT-US03-02358-36
6	27	1.0	60	5	US-09-911-261B-36
7	27	1.0	60	6	US-09-911-261A-36
8	26.8	1.0	51	5	US-09-749-280B-5554
9	26.8	1.0	51	5	US-09-749-280B-6407
10	26.6	1.0	56	1	PCT-US03-02358-49
11	26.6	1.0	56	5	US-09-911-261B-49
12	26.6	1.0	56	6	US-09-911-261A-49
13	25.8	0.9	60	1	PCT-US03-02358-45
14	25.8	0.9	60	5	US-09-911-261B-45
15	25.8	0.9	60	6	US-09-911-261A-45
16	25.6	0.9	56	1	PCT-US03-02358-40
17	25.6	0.9	56	5	US-09-911-261B-40
18	25.6	0.9	56	6	US-09-911-261A-40
19	25.2	0.9	50	9	US-10-325-899-2511
20	25.2	0.9	50	9	US-10-325-899-3660
21	25.2	0.9	51	5	US-09-749-280B-519
22	24.6	0.9	55	1	PCT-US03-02358-50

23	24.6	0.9	55	5	US-09-911-261B-50	Sequence 50, App1
24	24.6	0.9	55	6	US-09-911-261A-50	Sequence 50, App1
25	24.4	0.9	51	5	US-09-749-280B-5867	Sequence 5867, App
26	24.4	0.9	51	5	US-09-749-280B-6408	Sequence 6408, App
27	23.8	0.9	55	1	PCT-US03-02358-41	Sequence 41, App1
28	23.8	0.9	55	5	US-09-911-261B-41	Sequence 41, App1
29	23.8	0.9	55	6	US-09-911-261A-41	Sequence 41, App1
30	23.8	0.9	58	6	US-10-310-156A-470	Sequence 470, App
31	23.8	0.9	58	9	US-10-310-156B-470	Sequence 470, App
32	23	0.8	59	6	US-09-912-293-732	Sequence 732, App
33	22.4	0.8	41	11	US-60-449-155-516	Sequence 516, App
34	22.4	0.8	60	1	PCT-US03-02358-39	Sequence 39, App1
35	22.4	0.8	60	1	PCT-US03-02358-48	Sequence 48, App1
36	22.4	0.8	60	5	US-09-911-261B-39	Sequence 39, App1
37	22.4	0.8	60	5	US-09-911-261B-48	Sequence 48, App1
38	22.4	0.8	60	6	US-09-911-261A-39	Sequence 39, App1
39	22.4	0.8	60	6	US-09-911-261A-48	Sequence 48, App1
40	22.2	0.8	51	5	US-09-749-280B-6410	Sequence 6410, App
41	21.8	0.8	25	11	US-60-427-808-134357	Sequence 134357, App
42	21.8	0.8	25	11	US-60-427-836-480873	Sequence 480873, App
43	21.8	0.8	41	11	US-60-449-155-517	Sequence 517, App
44	21.8	0.8	60	9	US-10-257-848-81	Sequence 81, App1
45	21.8	0.8	60	9	US-10-325-899-4332	Sequence 4332, App
46	21.6	0.8	50	9	US-09-749-280B-5462	Sequence 5462, App
47	21.4	0.8	50	9	US-10-325-899-4844	Sequence 4844, App
48	21.4	0.8	50	5	US-09-749-280B-1151	Sequence 1151, App
49	21.2	0.8	50	8	US-10-089-560-10	Sequence 10, App1
50	21.2	0.8	50	9	US-10-325-899-4458	Sequence 4458, App
51	21.2	0.8	50	9	PCT-US03-02358-56	Sequence 56, App1
52	21	0.8	45	5	US-09-911-261B-56	Sequence 56, App1
53	21	0.8	45	6	US-09-911-261A-56	Sequence 56, App1
54	21	0.8	48	8	US-10-402-954-19	Sequence 19, App1
55	21	0.8	50	5	US-09-749-280B-5461	Sequence 5461, App
56	21	0.8	52	4	US-08-906-156A-72	Sequence 72, App1
57	21	0.8	53	4	US-08-906-156B-72	Sequence 72, App1
58	21	0.8	53	6	US-09-912-293-243046	Sequence 243046, App
59	21	0.8	59	8	US-09-912-293-2216	Sequence 2216, App
60	21	0.8	25	11	US-60-427-808-134407	Sequence 134407, App
61	20.8	0.8	25	11	US-10-325-899-1400	Sequence 1400, App
62	20.8	0.8	51	5	US-09-749-280B-522	Sequence 522, App
63	20.8	0.8	51	6	US-09-912-293-62705	Sequence 62705, App
64	20.8	0.8	56	6	US-09-912-293-153178	Sequence 153178, App
65	20.8	0.8	56	6	US-09-912-293-243169	Sequence 243169, App
66	20.6	0.7	27	1	PCT-US03-05186-47	Sequence 47, App1
67	20.6	0.7	51	5	US-09-749-280B-1308	Sequence 1308, App
68	20.6	0.7	51	5	US-09-749-280B-2579	Sequence 2579, App
69	20.6	0.7	52	8	US-10-409-627-244	Sequence 244, App
70	20.6	0.7	56	6	US-09-912-293-89289	Sequence 89289, App
71	20.6	0.7	60	8	US-10-193-926A-16	Sequence 16, App1
72	20.6	0.7	60	9	US-10-193-747-25	Sequence 25, App1
73	20.6	0.7	60	9	US-10-193-747-26	Sequence 26, App1
74	20.6	0.7	60	9	US-10-316-954-1179	Sequence 1179, App
75	20.6	0.7	60	9	US-10-316-954-2828	Sequence 2828, App
76	20.6	0.7	60	9	US-10-349-781-19132	Sequence 19132, App
77	20.6	0.7	49	8	US-10-287-787-7960	Sequence 7660, App
78	20.4	0.7	50	5	US-09-749-280B-1163	Sequence 3163, App
79	20.4	0.7	50	8	US-10-287-787-7659	Sequence 7659, App
80	20.4	0.7	50	9	US-10-325-899-201	Sequence 201, App
81	20.4	0.7	51	1	PCT-US03-0069A-13	Sequence 13, App1
82	20.4	0.7	51	5	US-09-749-280B-844	Sequence 844, App
83	20.4	0.7	52	7	US-09-837-604A-49233	Sequence 49233, App
84	20.4	0.7	25	11	US-60-427-808-134358	Sequence 134358, App
85	20.2	0.7	25	11	US-60-427-808-453684	Sequence 453684, App
86	20.2	0.7	25	11	US-60-427-808-453687	Sequence 453687, App
87	20.2	0.7	25	11	US-60-427-808-872650	Sequence 872650, App
88	20.2	0.7	25	11	US-60-427-836-289684	Sequence 289684, App
89	20.2	0.7	25	11	US-60-427-836-480872	Sequence 480872, App
90	20.2	0.7	25	11	US-60-427-836-500278	Sequence 500278, App
91	20.2	0.7	45	9	US-10-321-853-250	Sequence 250, App
92	20.2	0.7	47	9	US-10-349-143-201	Sequence 201, App
93	20.2	0.7	50	5	US-09-749-280B-2146	Sequence 2146, App
94	20.2	0.7	50	9	US-10-325-899-1747	Sequence 1747, App
95	20.2	0.7	50	9		

96	20.2	0.7	50	9	US-10-325-899-2954	Sequence 2954, Ap	C 169	19.4	0.7	56	6	US-09-912-293-189098	Sequence 189098,
C 97	20.2	0.7	50	9	US-10-325-899-6159	Sequence 6159, Ap	C 170	19.4	0.7	56	9	US-10-136-159A-106	Sequence 106, App
C 98	20.2	0.7	50	9	US-10-325-899-6222	Sequence 6222, Ap	C 171	19.4	0.7	57	1	PCT-US02-40891-975	Sequence 975, App
C 99	20.2	0.7	50	9	US-10-325-899-6355	Sequence 6355, Ap	C 172	19.4	0.7	57	1	PCT-US02-40891-977	Sequence 977, App
100	20.2	0.7	50	9	US-10-325-899-7334	Sequence 7334, Ap	C 173	19.4	0.7	57	1	PCT-US02-40892-307	Sequence 307, App
C 101	20.2	0.7	50	9	US-10-325-899-7546	Sequence 7546, Ap	C 174	19.4	0.7	57	1	PCT-US02-40892-309	Sequence 309, App
C 102	20.2	0.7	51	5	US-09-749-2808-1282	Sequence 1282, Ap	C 175	19.4	0.7	57	1	PCT-US02-40892A-307	Sequence 307, App
C 103	20.2	0.7	51	5	US-09-749-2808-3411	Sequence 3411, Ap	C 176	19.4	0.7	57	1	PCT-US02-40892A-309	Sequence 309, App
C 104	20.2	0.7	57	9	US-10-321-853-297	Sequence 297, App	C 177	19.4	0.7	57	8	US-10-287-787-3416	Sequence 3416, App
C 105	20.2	0.7	60	8	US-10-384-850-16	Sequence 16, App	C 178	19.4	0.7	60	1	PCT-US03-0412-56	Sequence 3416, App
106	20.2	0.7	60	11	US-60-288-292-4771	Sequence 4771, Ap	C 179	19.4	0.7	60	6	US-09-534-841-16126	Sequence 58, App
107	20	0.7	47	9	US-10-316-957-279	Sequence 279, App	C 180	19.2	0.7	25	6	US-09-866-108A-14627	Sequence 16126, A
C 108	20	0.7	47	9	US-10-316-957-280	Sequence 280, App	C 181	19.2	0.7	25	6	US-09-866-108A-14628	Sequence 14628, A
C 109	20	0.7	47	9	US-10-316-957-281	Sequence 281, App	C 182	19.2	0.7	25	11	US-60-427-808-72571	Sequence 14628, A
C 110	20	0.7	51	5	US-09-749-2808-535	Sequence 535, App	C 183	19.2	0.7	25	11	US-60-427-808-72571	Sequence 72571, A
C 111	19.8	0.7	25	6	US-09-660-222-139796	Sequence 139796,	C 184	19.2	0.7	25	11	US-60-427-808-72571	Sequence 134409
C 112	19.8	0.7	25	6	US-10-355-577-911174	Sequence 911174,	C 185	19.2	0.7	25	11	US-60-427-808-336016	Sequence 336016,
C 113	19.8	0.7	25	11	US-60-427-808-8553	Sequence 8553, Ap	C 186	19.2	0.7	25	11	US-60-427-808-336017	Sequence 336017,
114	19.8	0.7	25	11	US-60-427-808-142838	Sequence 142838,	C 187	19.2	0.7	25	11	US-60-427-808-440447	Sequence 440447,
115	19.8	0.7	25	11	US-60-427-808-452331	Sequence 452331,	C 188	19.2	0.7	25	11	US-60-427-808-601832	Sequence 601832,
C 116	19.8	0.7	25	11	US-60-427-808-432333	Sequence 432333,	C 189	19.2	0.7	25	11	US-60-427-808-766984	Sequence 766984,
C 117	19.8	0.7	25	11	US-60-427-808-820370	Sequence 820370,	C 190	19.2	0.7	25	11	US-60-427-808-770573	Sequence 770573,
C 118	19.8	0.7	25	11	US-60-427-836-118717	Sequence 118717,	C 191	19.2	0.7	25	11	US-60-427-808-861714	Sequence 861714,
C 119	19.8	0.7	40	8	US-10-287-787-21150	Sequence 21150, A	C 192	19.2	0.7	25	11	US-60-427-808-903557	Sequence 903557,
C 120	19.8	0.7	47	9	US-10-349-143-1468	Sequence 1468, A	C 193	19.2	0.7	25	11	US-60-427-808-903557	Sequence 903557,
C 121	19.8	0.7	47	9	US-10-333-429-165	Sequence 165, App	C 194	19.2	0.7	41	11	US-60-449-155-512	Sequence 276629,
C 122	19.8	0.7	50	5	US-09-749-2808-4178	Sequence 4178, App	C 195	19.2	0.7	41	11	US-10-349-143-802	Sequence 512, App
C 123	19.8	0.7	50	5	US-10-325-899-2798	Sequence 2798, Ap	C 196	19.2	0.7	47	9	US-10-349-143-1486	Sequence 802, App
C 124	19.8	0.7	50	9	US-10-325-899-4602	Sequence 4602, Ap	C 197	19.2	0.7	47	9	US-10-349-143-2536	Sequence 1486, Ap
C 125	19.8	0.7	50	9	US-10-325-899-7294	Sequence 7294, Ap	C 198	19.2	0.7	47	9	US-10-349-143-2859	Sequence 2536, Ap
C 126	19.8	0.7	51	1	PCT-US03-00669A-17	Sequence 17, App	C 199	19.2	0.7	47	9	US-10-349-143-2859	Sequence 2859, Ap
C 127	19.8	0.7	51	5	US-09-749-2808-257	Sequence 257, App	C 200	19.2	0.7	47	9	US-10-349-143-3534	Sequence 3534, Ap
C 128	19.8	0.7	51	5	US-09-749-2808-6113	Sequence 6113, Ap	C 201	19.2	0.7	49	11	US-10-349-143-3766	Sequence 3766, Ap
C 129	19.8	0.7	57	6	US-09-500-700-47	Sequence 47, App	C 202	19.2	0.7	50	5	US-60-288-282-38178	Sequence 38178, A
C 130	19.8	0.7	57	11	US-60-449-055-23	Sequence 23, App	C 203	19.2	0.7	50	5	US-09-749-2808-7215	Sequence 1474, Ap
C 131	19.8	0.7	58	5	US-09-513-999C-18026	Sequence 18026, A	C 204	19.2	0.7	50	5	US-10-325-899-853	Sequence 7215, Ap
C 132	19.8	0.7	58	6	US-09-513-999C-18026	Sequence 18026, A	C 205	19.2	0.7	50	9	US-10-325-899-853	Sequence 853, App
C 133	19.8	0.7	58	8	US-10-287-787-10059	Sequence 10059, A	C 206	19.2	0.7	50	9	US-10-325-899-2847	Sequence 2847, Ap
C 134	19.8	0.7	58	8	US-10-287-787-10201	Sequence 10201, A	C 207	19.2	0.7	50	9	US-10-325-899-3021	Sequence 3021, Ap
C 135	19.8	0.7	58	8	US-10-287-787-14769	Sequence 14769, A	C 208	19.2	0.7	51	5	US-09-749-2808-3794	Sequence 3794, Ap
C 136	19.8	0.7	60	9	US-10-329-624-1661	Sequence 1661, Ap	C 209	19.2	0.7	51	5	US-09-749-2808-882	Sequence 882, App
C 137	19.6	0.7	47	9	US-10-349-143-1231	Sequence 1231, Ap	C 210	19.2	0.7	51	6	US-09-922-225A-111	Sequence 2734, Ap
C 138	19.6	0.7	47	9	US-10-349-143-3797	Sequence 3797, Ap	C 211	19.2	0.7	51	6	US-09-922-225A-111	Sequence 111, App
C 139	19.6	0.7	48	6	US-09-863-041-3163	Sequence 3163, Ap	C 212	19.2	0.7	57	6	US-09-912-293-199375	Sequence 199375,
C 140	19.6	0.7	48	6	US-09-863-041A-3163	Sequence 3163, Ap	C 213	19.2	0.7	57	6	US-10-198-069-30	Sequence 30, App
C 141	19.6	0.7	50	9	US-10-325-899-3298	Sequence 3298, Ap	C 214	19.2	0.7	58	1	PCT-US03-14114-2821	Sequence 2821, Ap
C 142	19.6	0.7	50	9	US-10-325-899-3347	Sequence 3347, Ap	C 215	19.2	0.7	58	1	PCT-US03-14114-2822	Sequence 2822, Ap
C 143	19.6	0.7	51	5	US-09-749-2808-3132	Sequence 3132, Ap	C 216	19.2	0.7	58	1	PCT-US03-14114-2823	Sequence 2823, Ap
C 144	19.6	0.7	51	5	US-09-749-2808-5866	Sequence 5866, Ap	C 217	19.2	0.7	59	6	US-09-677-653A-53	Sequence 53, App
C 145	19.6	0.7	51	5	US-09-749-2808-6197	Sequence 6197, Ap	C 218	19.2	0.7	59	6	US-09-677-653A-53	Sequence 53, App
C 146	19.6	0.7	51	5	US-09-749-2808-6197	Sequence 6197, Ap	C 219	19.2	0.7	59	6	US-09-912-293-42307	Sequence 42307, A
C 147	19.6	0.7	58	9	US-10-102-143-30	Sequence 30, App	C 220	19.2	0.7	60	11	US-60-422-176-685	Sequence 50706, A
C 148	19.4	0.7	43	6	US-09-136-159-99	Sequence 99, App	C 221	19	0.7	30	6	US-09-980-559-31	Sequence 685, App
C 149	19.4	0.7	43	6	US-09-136-159-99	Sequence 99, App	C 222	19	0.7	30	6	US-09-785-632B-80	Sequence 31, App
C 150	19.4	0.7	43	6	US-09-136-159A-99	Sequence 99, App	C 223	19	0.7	45	8	US-10-257-549-53	Sequence 80, App
C 151	19.4	0.7	45	1	PCT-US02-38450-163	Sequence 163, App	C 224	19	0.7	47	9	US-10-349-143-1679	Sequence 53, App
C 152	19.4	0.7	45	1	PCT-US03-02358-54	Sequence 54, App	C 225	19	0.7	48	5	US-09-911-2618-43	Sequence 1679, Ap
C 153	19.4	0.7	45	5	US-09-911-261B-54	Sequence 54, App	C 226	19	0.7	48	5	US-09-911-2618-43	Sequence 43, App
C 154	19.4	0.7	47	9	US-10-349-143-1304	Sequence 54, App	C 227	19	0.7	48	6	US-09-911-2618-43	Sequence 43, App
C 155	19.4	0.7	47	9	US-10-349-143-1304	Sequence 54, App	C 228	19	0.7	48	6	US-09-911-2618-43	Sequence 43, App
C 156	19.4	0.7	48	8	US-10-367-892-6822	Sequence 1304, Ap	C 229	19	0.7	50	1	PCT-US03-13015-596	Sequence 596, App
C 157	19.4	0.7	49	11	US-60-288-292-10249	Sequence 6822, Ap	C 230	19	0.7	50	5	US-09-749-2808-7164	Sequence 7164, Ap
C 158	19.4	0.7	50	9	US-09-749-2808-1274	Sequence 1274, Ap	C 231	19	0.7	50	6	US-09-749-2808-7362	Sequence 7362, Ap
C 159	19.4	0.7	50	9	US-10-325-899-2323	Sequence 2323, Ap	C 232	19	0.7	50	6	US-09-906-777B-57	Sequence 57, App
C 160	19.4	0.7	50	9	US-10-325-899-3870	Sequence 3870, Ap	C 233	19	0.7	50	6	US-09-904-011C-57	Sequence 57, App
C 161	19.4	0.7	50	9	US-10-325-899-3870	Sequence 3870, Ap	C 234	19	0.7	50	6	US-09-904-011C-57	Sequence 57, App
C 162	19.4	0.7	51	5	US-09-749-2808-2318	Sequence 2318, Ap	C 235	19	0.7	50	8	US-10-426-504-57	Sequence 57, App
C 163	19.4	0.7	51	5	US-09-749-2808-2318	Sequence 2318, Ap	C 236	19	0.7	50	8	US-10-426-504-57	Sequence 57, App
C 164	19.4	0.7	54	6	US-09-912-293-219013	Sequence 3575, Ap	C 237	19	0.7	50	8	US-10-427-239-57	Sequence 57, App
C 165	19.4	0.7	54	8	US-10-287-919-1217	Sequence 219013,	C 238	19	0.7	50	8	US-10-426-504-57	Sequence 57, App
C 166	19.4	0.7	54	8	US-10-287-919-1217	Sequence 1217, Ap	C 239	19	0.7	50	9	US-10-426-504-57	Sequence 57, App
C 167	19.4	0.7	56	6	US-09-136-159-106	Sequence 1217, Ap	C 240	19	0.7	50	9	US-10-299-976-57	Sequence 57, App
C 168	19.4	0.7	56	6	US-09-136-159A-106	Sequence 106, App	C 241	19	0.7	50	9	US-10-298-993-57	Sequence 57, App
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ALIGNMENTS

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RESULT 1
US-09-749-280B-127
: Sequence 127, Application US/09749280B
: GENERAL INFORMATION:
: APPLICANT: Shinkets, Richard A.
: TITLE OF INVENTION: Nucleic Acids Containing Single
: FILE REFERENCE: 15966-610
: CURRENT APPLICATION NUMBER: US/09/749, 280B
: PRIOR FILING DATE: 2000-12-27
: PRIORITY APPLICATION NUMBER: 60/173,419
: NUMBER OF SEQ ID NOS: 10038
: SOFTWARE: Curagen Patent Formatter Version 0.9
: SEQ ID NO 127
: LENGTH: 51
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: allele
: LOCATION: (26)..(0)
: OTHER INFORMATION: single nucleotide polymorphism
: FEATURE:
: NAME/KEY: misc.feature
: LOCATION: (0)..(0)
: OTHER INFORMATION: Accession number cg44031583
US-09-749-280B-127
```


;; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
;; FILE REFERENCE: 109845.158
;; CURRENT APPLICATION NUMBER: PCT/US03/023358
;; CURRENT FILING DATE: 2003-01-23
;; PRIOR APPLICATION NUMBER: US 10/057,408
;; PRIOR FILING DATE: 2002-01-23
;; NUMBER OF SEQ ID NOS: 87
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 36
;; LENGTH: 60
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Partial zinc finger domain oligomer
;; NAME/KEY: misc_feature
;; LOCATION: (45)..(56)
;; OTHER INFORMATION: Nucleotides 45-47 and 51-56 are "n" wherein "n" = g, a, t, or c.
PCT-US03-023358-36

Query Match 1.0%: Score 27; DB 1; Length 60;
Best Local Similarity 60.0%: Pred. No. 2.9e+03;
Matches 36: Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1593 GGGGAGAACCCATTGTATGTACGAGTGGGCGGCGCTTTACCCGGAATCAACCCCTG.1652
Db 1 GGGGAGAACCCGCTATAATGTCCGGAATGTGCTAAAGTTTACGNNNAGCNNNNNTTG 50

RESULT 6
US-09-911-261B-36
;; Sequence 36, Application US/09911261B
;; GENERAL INFORMATION:
;; APPLICANT: Sera, Takashi
;; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
;; FILE REFERENCE: 109845.135
;; CURRENT APPLICATION NUMBER: US/09/911,261B
;; CURRENT FILING DATE: 2000-07-21
;; PRIOR APPLICATION NUMBER: US 60/220,060
;; PRIOR FILING DATE: 2000-07-21
;; NUMBER OF SEQ ID NOS: 69
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 36
;; LENGTH: 60
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Partial zinc finger domain oligomer
;; NAME/KEY: misc_feature
;; LOCATION: (45)..(56)
;; OTHER INFORMATION: Nucleotides 45-47 and 51-56 are "n" wherein "n" = g, a, t, or c.
US-09-911-261B-36

Query Match 1.0%: Score 27; DB 5; Length 60;
Best Local Similarity 60.0%: Pred. No. 2.9e+03;
Matches 36: Conservative 0; Mismatches 24; Indels 0; Gaps 0;

OY 1593 GGGGAGAACCCATTGTATGTACGAGTGGGCGGCGCTTTACCCGGAATCAACCCCTG 1652
Db 1 GGGGAGAACCCGCTATAATGTCCGGAATGTGCTAAAGTTTACGNNNAGCNNNNNTTG 60

RESULT 7
US-09-911-261A-36
;; Sequence 36, Application US/09911261A
;; GENERAL INFORMATION:
;; APPLICANT: Sera, Takashi
;; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
;; FILE REFERENCE: 109845.135
;; CURRENT APPLICATION NUMBER: US/09/911,261A
;; CURRENT FILING DATE: 2001-07-23
;; PRIOR APPLICATION NUMBER: US 60/220,060

;; PRIOR FILING DATE: 2000-07-21
;; NUMBER OF SEQ ID NOS: 69
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 36
;; LENGTH: 60
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Partial zinc finger domain oligomer
;; NAME/KEY: misc_feature
;; LOCATION: (45)..(56)
;; OTHER INFORMATION: Nucleotides 45-47 and 51-56 are "n" wherein "n" = g, a, t, or c.
US-09-911-261A-36

Query Match 1.0%: Score 27; DB 6; Length 60;
Best Local Similarity 60.0%: Pred. No. 2.9e+03;
Matches 36: Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1593 GGGGAGAACCCATTGTATGTACGAGTGGGCGGCGCTTTACCCGGAATCAACCCCTG 1652
Db 1 GGGGAGAACCCGCTATAATGTCCGGAATGTGCTAAAGTTTACGNNNAGCNNNNNTTG 60

RESULT 8
US-09-749-280B-5554
;; Sequence 5554, Application US/09749280B
;; GENERAL INFORMATION:
;; APPLICANT: Shimkets, Richard A.
;; TITLE OF INVENTION: Nucleic Acids Containing Single
;; FILE REFERENCE: 15966-610
;; CURRENT APPLICATION NUMBER: US/09/749,280B
;; CURRENT FILING DATE: 2000-12-27
;; PRIOR APPLICATION NUMBER: 60/173,419
;; PRIOR FILING DATE: 1999-12-28
;; NUMBER OF SEQ ID NOS: 10038
;; SOFTWARE: Curagen Patent Formatter Version 0.9
;; SEQ ID NO 5554
;; LENGTH: 51
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: allele
;; LOCATION: (26)..(0)
;; OTHER INFORMATION: single nucleotide polymorphism
;; NAME/KEY: misc_feature
;; LOCATION: (0)..(0)
;; OTHER INFORMATION: Accession number c943959535
US-09-749-280B-5554

Query Match 1.0%: Score 26.8; DB 5; Length 51;
Best Local Similarity 73.9%: Pred. No. 3.1e+03;
Matches 34: Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 214 TGACATTCAGGATGTGCTGTACTTACCCCGAGGAGGTGAG 259
Db 1 TGACTTTGAAGACGTGCTGTGCAATTTTCCAGGAGATGAG 46

RESULT 9
US-09-749-280B-6407
;; Sequence 6407, Application US/09749280B
;; GENERAL INFORMATION:
;; APPLICANT: Shimkets, Richard A.
;; TITLE OF INVENTION: Nucleic Acids Containing Single
;; FILE REFERENCE: 15966-610
;; CURRENT APPLICATION NUMBER: US/09/749,280B
;; CURRENT FILING DATE: 2000-12-27

```
; PRIOR APPLICATION NUMBER: 60/173,419
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 10038
; SOFTWARE: Curagen Patent Formatter Version 0.9
; SEQ ID NO 6407
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: (26)...(0)
; OTHER INFORMATION: single nucleotide polymorphism
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Accession number cg43051067
; US-09-749-280B-6407

Query Match
Best Local Similarity 1.0%; Score 26.8; DB 5; Length 51;
Matches 34; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 1560 TCAAACTTAAACAACACGAGGTCAACACAGGGGAGAGCCAT 1605
Db 1 TCAAACTGACATCCACGACGAGAACACACAGGAGAGGCCCT 46

RESULT 10
PCT-US03-02358-49
; Sequence 49, Application PC/TUS0302358
; GENERAL INFORMATION:
; APPLICANT: Sera, Takashi
; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
; FILE REFERENCE: 109845.158
; CURRENT APPLICATION NUMBER: PCT/US03/02358
; CURRENT FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: US 10/057,408
; PRIOR FILING DATE: 2002-01-23
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49
; LENGTH: 56
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Partial zinc finger domain oligomer
PCT-US03-02358-49

Query Match
Best Local Similarity 1.0%; Score 26.6; DB 1; Length 56;
Matches 35; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 921 GGGGAGACACCTTACATGTACACTGAGTGGGAGAGACGCTTTGGCAGTA 969
Db 1 GGGGAGAACCTTACAAAGTGCCCTGAATGCGGAAGAGCTTTAGTCGTA 49

RESULT 11
US-09-911-261B-49
; Sequence 49, Application US/09911261B
; GENERAL INFORMATION:
; APPLICANT: Sera, Takashi
; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
; FILE REFERENCE: 109845.155
; CURRENT APPLICATION NUMBER: US/09/911,261B
; CURRENT FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/220,060
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 49
; LENGTH: 56
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Partial zinc finger domain oligomer
US-09-911-261B-49

Query Match
Best Local Similarity 1.0%; Score 26.6; DB 5; Length 56;
Matches 35; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 921 GGGGAGACACCTTACATGTACACTGAGTGGGAGAGACGCTTTGGCAGTA 969
Db 1 GGGGAGAACCTTACAAAGTGCCCTGAATGCGGAAGAGCTTTAGTCGTA 49

RESULT 12
US-09-911-261A-49
; Sequence 49, Application US/09911261A
; GENERAL INFORMATION:
; APPLICANT: Sera, Takashi
; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
; FILE REFERENCE: 109845.135
; CURRENT APPLICATION NUMBER: US/09/911,261A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/220,060
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 49
; LENGTH: 56
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Partial zinc finger domain oligomer
US-09-911-261A-49

Query Match
Best Local Similarity 1.0%; Score 26.6; DB 6; Length 56;
Matches 35; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 921 GGGGAGACACCTTACATGTACACTGAGTGGGAGAGACGCTTTGGCAGTA 969
Db 1 GGGGAGAACCTTACAAAGTGCCCTGAATGCGGAAGAGCTTTAGTCGTA 49

RESULT 13
PCT-US03-02358-45
; Sequence 45, Application PC/TUS0302358
; GENERAL INFORMATION:
; APPLICANT: Sera, Takashi
; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
; FILE REFERENCE: 109845.158
; CURRENT APPLICATION NUMBER: PCT/US03/02358
; CURRENT FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: US 10/057,408
; PRIOR FILING DATE: 2002-01-23
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Partial zinc finger domain oligomer
PCT-US03-02358-45

Query Match
Best Local Similarity 0.9%; Score 25.8; DB 1; Length 60;
Matches 33; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 1593 GGGGAGAACCATTTGATGTACGAGAGTGCGGCGAGGCGCTTTAC 1637
Db 1 GGGGAGAACCCGTATTAATGTCCGGAATGTGTAAGTTTACG 45
```

```

RESULT 14
US-09-911-261B-45
; Sequence 45, Application US/09911261B
; GENERAL INFORMATION:
; APPLICANT: Sera, Takashi
; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
; FILE REFERENCE: 109845.135
; CURRENT APPLICATION NUMBER: US/09/911,261B
; CURRENT FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/220,060
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Partial zinc finger domain oligomer
US-09-911-261B-45

```

```

Query Match
Best Local Similarity 0.9%; Score 25.8; DB 5; Length 60;
Matches 33; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

```

```

QY 1593 GGGGAGAACCCATTGTGTATGACGAGTGTGGCGAGCCTTTACC 1637
DB 1 GGGGAGAACCCGCTAATAATGTCGGAATGTGTAAGTTTACG 45

```

```

RESULT 15
US-09-911-261A-45
; Sequence 45, Application US/09911261A
; GENERAL INFORMATION:
; APPLICANT: Sera, Takashi
; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
; FILE REFERENCE: 109845.135
; CURRENT APPLICATION NUMBER: US/09/911,261A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/220,060
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Partial zinc finger domain oligomer
US-09-911-261A-45

```

```

Query Match
Best Local Similarity 0.9%; Score 25.8; DB 6; Length 60;
Matches 33; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

```

```

QY 1593 GGGGAGAACCCATTGTGTATGACGAGTGTGGCGAGCCTTTACC 1637
DB 1 GGGGAGAACCCGCTAATAATGTCGGAATGTGTAAGTTTACG 45

```

```

RESULT 16
PCT-US03-02358-40
; Sequence 40, Application PC/TUS0302358
; GENERAL INFORMATION:
; APPLICANT: Sera, Takashi
; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
; FILE REFERENCE: 109845.138
; CURRENT APPLICATION NUMBER: PCT/US03/02358
; CURRENT FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: US 10/057,408
; PRIOR FILING DATE: 2002-01-23
; NUMBER OF SEQ ID NOS: 87

```

```

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 56
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Partial zinc finger domain oligomer
; NAME/KEY: misc_feature
; LOCATION: (48)..(58)
; OTHER INFORMATION: Nucleotides 48-50 and 54-58 are "n" wherein "n" = g, a, t, or
PCT-US03-02358-40

```

```

Query Match
Best Local Similarity 0.9%; Score 25.6; DB 1; Length 56;
Matches 31; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

```

```

QY 1179 AAGCCTTATGTGTGCAAGCAATGTGGCGACAGCTTTAGCCTGA 1221
DB 7 AAGCCTTACAGTGCCTGATGCGGAGAGACCTTTAGTNNNA 49

```

```

RESULT 17
US-09-911-261B-40
; Sequence 40, Application US/09911261B
; GENERAL INFORMATION:
; APPLICANT: Sera, Takashi
; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
; FILE REFERENCE: 109845.135
; CURRENT APPLICATION NUMBER: US/09/911,261B
; CURRENT FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/220,060
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 40
; LENGTH: 56
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Partial zinc finger domain oligomer
; NAME/KEY: misc_feature
; LOCATION: (48)..(58)
; OTHER INFORMATION: Nucleotides 48-50 and 54-58 are "n" wherein "n" = g, a, t, or
US-09-911-261B-40

```

```

Query Match
Best Local Similarity 0.9%; Score 25.6; DB 5; Length 56;
Matches 31; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

```

```

QY 1179 AAGCCTTATGTGTGCAAGCAATGTGGCGACAGCTTTAGCCTGA 1221
DB 7 AAGCCTTACAGTGCCTGATGCGGAGAGACCTTTAGTNNNA 49

```

```

RESULT 18
US-09-911-261A-40
; Sequence 40, Application US/09911261A
; GENERAL INFORMATION:
; APPLICANT: Sera, Takashi
; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
; FILE REFERENCE: 109845.135
; CURRENT APPLICATION NUMBER: US/09/911,261A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/220,060
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 40
; LENGTH: 56
; TYPE: DNA
; ORGANISM: Artificial Sequence

```

```
FEATURE:
OTHER INFORMATION: Partial zinc finger domain oligomer
FEATURE:
NAME/KEY: misc_feature
LOCATION: (48)..(58)
OTHER INFORMATION: Nucleotides 48-50 and 54-58 are "n" wherein "n" = g, a, t, or c.
US-09-911-261A-40
```

```
Query Match          0.9%: Score 25.6; DB 6; Length 56;
Best Local Similarity 72.1%; Pred. No. 7.1e+03;
Matches 31; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
```

```
QY 1179 AAGCCTTATGTGTCAGAGATGTGGCAGAGCTTTAGCCTGA 1221
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 7 AAGCCTTACAAGTGCCTGAATGCGGAGAGAGCTTGTGTTNNA 49
```

```
RESULT 19
US-10-325-899-2511
Sequence 2511, Application US/10325899
GENERAL INFORMATION:
APPLICANT: Wohlgenuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Ly, Ngoc
APPLICANT: Woodward, Robert
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING TRANSPLANT
FILE REFERENCE: 506612000122
CURRENT APPLICATION NUMBER: US/10/325,899
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
NUMBER OF SEQ ID NOS: 9966
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2511
LENGTH: 50
TYPE: DNA
ORGANISM: Homo sapiens
US-10-325-899-2511
```

```
Query Match          0.9%: Score 25.2; DB 9; Length 50;
Best Local Similarity 71.7%; Pred. No. 8.9e+03;
Matches 33; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
```

```
QY 1547 CTTAGCCTGAAGTCAACCTTACAAACACGAGGTCACACAG 1592
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4 CTTAGTCAGAGCTCAACCTTACAAACACGAGGTCACAGATTACATG 49
```

```
RESULT 20
US-10-325-899-3660
Sequence 3660, Application US/10325899
GENERAL INFORMATION:
APPLICANT: Wohlgenuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Ly, Ngoc
APPLICANT: Woodward, Robert
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING TRANSPLANT
FILE REFERENCE: 506612000122
CURRENT APPLICATION NUMBER: US/10/325,899
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
NUMBER OF SEQ ID NOS: 9966
```

```
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3660
LENGTH: 50
TYPE: DNA
ORGANISM: Homo sapiens
US-10-325-899-3660
```

```
Query Match          0.9%: Score 25.2; DB 9; Length 50;
Best Local Similarity 71.7%; Pred. No. 8.9e+03;
Matches 33; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
```

```
QY 1547 CTTAGCCTGAAGTCAACCTTACAAACACGAGGTCACACAG 1592
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4 CTTAGTCAGAGCTCAACCTTACAAACACGAGGTCACAGATTACATG 49
```

```
RESULT 21
US-09-749-280B-519
Sequence 519, Application US/09749280B
GENERAL INFORMATION:
APPLICANT: Shinkens, Richard A.
APPLICANT: Leach, Martin
TITLE OF INVENTION: Nucleic Acids Containing Single
FILE REFERENCE: 15966-610
CURRENT APPLICATION NUMBER: US/09/749,280B
CURRENT FILING DATE: 2000-12-27
PRIOR APPLICATION NUMBER: 60/173,419
PRIOR FILING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 10038
SOFTWARE: Curacen Patent Formatter Version 0.9
SEQ ID NO 519
LENGTH: 51
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: allele
LOCATION: (26)...(0)
OTHER INFORMATION: single nucleotide polymorphism
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Accession number c943051067
US-09-749-280B-519
```

```
Query Match          0.9%: Score 25.2; DB 5; Length 51;
Best Local Similarity 71.7%; Pred. No. 8.9e+03;
Matches 33; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
```

```
QY 1225 CAACCTCATTTACCAACGAGGCGGCGACACTGGGGAGAGCCTTA 1270
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 CAACCTGCACATCCACCAAGCGAGTTTCACACAGAGAGAGGCCCTA 46
```

```
RESULT 22
PCT-US03-02358-50/c
Sequence 50, Application PC/TUS0302358
GENERAL INFORMATION:
APPLICANT: Sera, Takashi
TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
FILE REFERENCE: 109845,158
CURRENT APPLICATION NUMBER: PCT/US03/02358
CURRENT FILING DATE: 2003-01-23
PRIOR APPLICATION NUMBER: US 10/057,408
PRIOR FILING DATE: 2002-01-23
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn version 3.2
SEQ ID NO 50
LENGTH: 55
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Partial zinc finger domain oligomer
```

PCT-US03-02358-50

Query Match
Best Local Similarity 0.9%; Score 24.6; DB 1; Length 55;
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Db 1211 CTTAGCCTGAAGTCAACCTCATTACCCACGAGGGCGCACACTGGGAGAG 1265
55 CTTAGTCGTAGTATAGCTTACAAACCCACGACGACGACGAGGAGAG 1

RESULT 23

US-09-911-261B-50/c
Sequence 50, Application US/09911261B
GENERAL INFORMATION:
APPLICANT: Sera, Takashi
TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
FILE REFERENCE: 109845.135
CURRENT APPLICATION NUMBER: US/09/911,261B
CURRENT FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: US 60/220,060
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PatentIn version 3.0
SEQ ID NO 50
LENGTH: 55
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Partial zinc finger domain oligomer
US-09-911-261B-50

Query Match
Best Local Similarity 0.9%; Score 24.6; DB 5; Length 55;
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Db 1211 CTTAGCCTGAAGTCAACCTCATTACCCACGAGGGCGCACACTGGGAGAG 1265
55 CTTAGTCGTAGTATAGCTTACAAACCCACGACGACGACGAGGAGAG 1

RESULT 24

US-09-911-261A-50/c
Sequence 50, Application US/09911261A
GENERAL INFORMATION:
APPLICANT: Sera, Takashi
TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
FILE REFERENCE: 109845.135
CURRENT APPLICATION NUMBER: US/09/911,261A
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 60/220,060
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PatentIn version 3.0
SEQ ID NO 50
LENGTH: 55
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Partial zinc finger domain oligomer
US-09-911-261A-50

Query Match
Best Local Similarity 0.9%; Score 24.6; DB 6; Length 55;
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Db 1211 CTTAGCCTGAAGTCAACCTCATTACCCACGAGGGCGCACACTGGGAGAG 1265
55 CTTAGTCGTAGTATAGCTTACAAACCCACGACGACGACGAGGAGAG 1

RESULT 25

US-09-749-280B-5867

Sequence 5867, Application US/09749280B

GENERAL INFORMATION:
APPLICANT: Shimkets, Richard A.
TITLE OF INVENTION: Nucleic Acids Containing Single
FILE REFERENCE: 15966-610
CURRENT APPLICATION NUMBER: US/09/749,280B
CURRENT FILING DATE: 2000-12-27
PRIOR APPLICATION NUMBER: 60/173,419
PRIOR FILING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 10038
SOFTWARE: Curagen Patent Formatter Version 0.9
SEQ ID NO 5867
LENGTH: 51
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: allele
LOCATION: (26)...(0)
OTHER INFORMATION: single nucleotide polymorphism
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Accession number c942532030
US-09-749-280B-5867

Query Match
Best Local Similarity 0.9%; Score 24.4; DB 5; Length 51;
Matches 34; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Db 1353 TACATTTCGAGGAGTGTGAGCAGCTTTACCCAGAGTCAACCTCAT 1402
1 TATAATGTGATGAGTGTGCGAAGCTTCACTCAGAGCTCAGATCTTAT 50

RESULT 26

US-09-749-280B-6408
Sequence 6408, Application US/09749280B
GENERAL INFORMATION:
APPLICANT: Shimkets, Richard A.
TITLE OF INVENTION: Nucleic Acids Containing Single
FILE REFERENCE: 15966-610
CURRENT APPLICATION NUMBER: US/09/749,280B
CURRENT FILING DATE: 2000-12-27
PRIOR APPLICATION NUMBER: 60/173,419
PRIOR FILING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 10038
SOFTWARE: Curagen Patent Formatter Version 0.9
SEQ ID NO 6408
LENGTH: 51
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: allele
LOCATION: (26)...(0)
OTHER INFORMATION: single nucleotide polymorphism
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Accession number c943051067
US-09-749-280B-6408

Query Match
Best Local Similarity 0.9%; Score 24.4; DB 5; Length 51;
Matches 34; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Db 1548 TTTAGCCTGAAGTCAACCTTACCAACACGAGGCTCAGACAGGAGGA 1597
1 TTACAGCAGAGCTCCACCTTACAGCCAGCGGGGTTCAAGAAAGA 50

RESULT 27
PCT-US03-02358-41/c
; Sequence 41, Application PC/TUS0302358
; GENERAL INFORMATION:
; APPLICANT: Seta, Takashi
; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
; FILE REFERENCE: 109845.158
; CURRENT APPLICATION NUMBER: PCT/US03/02358
; PRIOR FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: US 10/057,408
; PRIOR FILING DATE: 2002-01-23
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Partial zinc finger domain oligomer
; NAME/KEY: misc_feature
; LOCATION: (28)..(48)
; OTHER INFORMATION: Nucleotides 28-30, 37-42 and 46-48 are "n" wherein "n" =
; OTHER INFORMATION: g, a, t, or c
PCT-US03-02358-41

Query Match
Best Local Similarity 0.9%; Score 23.8; DB 1; Length 55;
Best Local Similarity 56.4%; Pred. No. 2.4e+04;
Matches 31; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1547 CTTAGCCTGAAGTCAACCTTAACAACACAGAGTCACACAGCGGGGAGAG 1601
Db 55 CTTAGTNNNAGTNNNNNTTACAAANNACCAACGACGACGCGGGGAGAG 1

RESULT 28
US-09-911-261B-41/c
; Sequence 41, Application US/09911261B
; GENERAL INFORMATION:
; APPLICANT: Seta, Takashi
; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
; FILE REFERENCE: 109845.135
; CURRENT APPLICATION NUMBER: US/09/911.261B
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/220,060
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Partial zinc finger domain oligomer
; NAME/KEY: misc_feature
; LOCATION: (28)..(48)
; OTHER INFORMATION: Nucleotides 28-30, 37-42 and 46-48 are "n" wherein "n" =
; OTHER INFORMATION: g, a, t, or c
US-09-911-261B-41

Query Match
Best Local Similarity 0.9%; Score 23.8; DB 5; Length 55;
Best Local Similarity 56.4%; Pred. No. 2.4e+04;
Matches 31; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1547 CTTAGCCTGAAGTCAACCTTAACAACACAGAGTCACACAGCGGGGAGAG 1601
Db 55 CTTAGTNNNAGTNNNNNTTACAAANNACCAACGACGACGCGGGGAGAG 1

RESULT 29
US-09-911-261A-41/c

; Sequence 41, Application US/09911261A
; GENERAL INFORMATION:
; APPLICANT: Seta, Takashi
; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
; FILE REFERENCE: 109845.135
; CURRENT APPLICATION NUMBER: US/09/911.261A
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/220,060
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Partial zinc finger domain oligomer
; NAME/KEY: misc_feature
; LOCATION: (28)..(48)
; OTHER INFORMATION: Nucleotides 28-30, 37-42 and 46-48 are "n" wherein "n" =
; OTHER INFORMATION: g, a, t, or c
US-09-911-261A-41

Query Match
Best Local Similarity 0.9%; Score 23.8; DB 6; Length 55;
Best Local Similarity 56.4%; Pred. No. 2.4e+04;
Matches 31; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1547 CTTAGCCTGAAGTCAACCTTAACAACACAGAGTCACACAGCGGGGAGAG 1601
Db 55 CTTAGTNNNAGTNNNNNTTACAAANNACCAACGACGACGCGGGGAGAG 1

RESULT 30
US-10-310-156A-470/c
; Sequence 470, Application US/10310156A
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Chlamydothila pneumoniae AR39, complete genome.
; FILE REFERENCE: Jim Zegeer law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/310.156A
; PRIOR FILING DATE: 2003-04-10
; NUMBER OF SEQ ID NOS: 742
; SOFTWARE: Proprietary
; SEQ ID NO 470
; LENGTH: 58
; TYPE: DNA
; ORGANISM: Chlamydothila pneumoniae AR39, complete genome.
; FEATURE:
; LOCATION: (827553)...(827610)
; OTHER INFORMATION: Chromosome = 1 strand = positive ConnectionObjectNumber =
US-10-310-156A-470

Query Match
Best Local Similarity 0.9%; Score 23.8; DB 8; Length 58;
Best Local Similarity 80.0%; Pred. No. 2.4e+04;
Matches 28; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2274 CTTGAGGAGATTCGCTGCTCATTTTCAGGAGCC 2308
Db 39 CTTGAGGAGGTTTCGCTGCTCCTCTGAGGAGCC 5

RESULT 31
US-10-310-156-470/c
; Sequence 470, Application US/10310156
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Chlamydothila pneumoniae AR39, complete genome.
; FILE REFERENCE: Jim Zegeer law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/310.156
; PRIOR FILING DATE: 2002-12-05
; NUMBER OF SEQ ID NOS: 742
; SOFTWARE: Proprietary


```

: TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
: FILE REFERENCE: 1098445.158
: CURRENT APPLICATION NUMBER: PCT/US03/02358
: CURRENT FILING DATE: 2003-01-23
: PRIOR APPLICATION NUMBER: US 10/057,408
: PRIOR FILING DATE: 2002-01-23
: NUMBER OF SEQ ID NOS: 87
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 48
: LENGTH: 60
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Partial zinc finger domain oligomer
PCT-US03-02358-48

```

			0.8%;	Score 22.4;	DB 1;	length 60;
Query Match						
Best Local Similarity			81.2%;	Pred. No.	6.3e-04;	
Matches	26;	Conservative	0;	Mismatches	6;	Indels
Gaps						0;
OY	1239	CACCGAGGGGCACTCAGGGAAGAACCCTTA	1270			
Dd	36	CATCAGCGTACTCACACTGGCCGACAAGCCTTA	5			

```

RESULT 36
US-09-911-261B-39/C
: Sequence 39, Application US/09911261B
: GENERAL INFORMATION:
: APPLICANT: Serz, Takashi
: TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
: FILE REFERENCE: 109845.135
: CURRENT APPLICATION NUMBER: US/09/911,261B
: PRIORITY FILING DATE: 2000-07-21
: PRIOR APPLICATION NUMBER: US 60/220,060
: PRIOR FILING DATE: 2000-07-21
: NUMBER OF SEQ ID NOS: 69
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 39
: LENGTH: 60
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Partial zinc finger domain oligomer
: FEATURE:
: NAME/KEY: misc.feature
: LOCATION: (37)-(51)
: OTHER INFORMATION: Nucleotides 37-39 and 46-51 are "n" wherein "n" = g, a, t, or c
US-09-911-261B-39

```

Query Match	0.8%	Score 22.4	DB 5	Length 60
Best Local Similarity	81.2%	Pred. No. 6.3e+04		
Matches	26	Conservative	0	Mismatches 6
				Indels 0
				Gaps 0
Q7	1239	CACCAAGAGGGCCACACCTGGGAGAGACCTTA	1270	
DB	36	CATCAGCGTACTCTCACACTGGGAGAGACCTTA	5	

```

: RESULT 37
: US-09-911-261B-48/c
: Sequence 48, Application US/09911261B
: GENERAL INFORMATION:
: APPLICANT: Sera, Takashi
: TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
: FILE REFERENCE: 109845.135
: CURRENT APPLICATION NUMBER: US/09/911,261B
: CURRENT FILING DATE: 2000-07-21
: PRIOR APPLICATION NUMBER: US 60/220,060
: PRIOR FILING DATE: 2000-07-21
: NUMBER OF SEQ ID NOS: 69
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 48

```

```

: LENGTH: 60
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Partial zinc finger domain oligomer
US-09-911-261B-48

```

Query Match	0.8%	Score	22.4	DB	5	Length	60
Best Local Similarity	81.2%	Pred. No.	6.3e+04				
Matches	26	Conservative	0	Mismatches	6	Indels	0
						Gaps	0

QY 1239 CACCAGAGGGCGCACACTGGGAGAGACCTTA 1270
 ||||| | ||||| |||||
 Db 36 CATCAGCGTACTCACACTGGCGAGAGAAGCCTTA 5

```

RESULT 38
US-09-911-261A-39/c
; Sequence 39, Application US/09911261A
; GENERAL INFORMATION:
; APPLICANT: Seta, Takashi
; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
; FILE REFERENCE: 109845.135
; CURRENT APPLICATION NUMBER: US/09/911,261A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/220,060
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 39
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Partial zinc finger domain oligomer
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (37)..(51)
; OTHER INFORMATION: Nucleotides 37-39 and 46-51 are "n" wherein "n" = g, a, t, or
US-09-911-261A-39

```

	Query Match	0.8%	Score 22.4;	DB 6;	Length 60;
	Best Local Similarity	81.2%;	Pred. No. 6.3e+04;		
	Matches	26; Conservative	0; Mismatches	6; Indels	0; Gaps
OY	1239	CACCCAGAGGGCGCACACTGTTGGGAGAGAACCCTTA	1270		
Db	36	CATCAGCGTACTTCACACTGTGGCGAGAGGCCCTTA	5		

RESULT 39 261A-48/c
US-09-911-261A-48/c
; Sequence 48, Application US/09911261A
; GENERAL INFORMATION:
; APPLICANT: Sere, Takashi
; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof

```

? PRIOR APPLICATION NUMBER: US 60/220,060
? PRIOR FILING DATE: 2000-07-21
? NUMBER OF SEQ ID NOS: 69
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 48
? LENGTH: 60
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Partial zinc finger domain oligomer
US-09-911-261A-48

```

Query Match	0.88;	Score 22.4;	DB 6;	Length 60;
Best Local Similarity	81.28;	Pred. No. 6.3e+04;		

Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1239 CACCAGAGCCGACACTGGGAGAACCTTA 1270
DB 36 CATCAGCTACTCAGACTGGCAGAGACCTTA 5

RESULT 40
US-09-749-280B-6410
; Sequence 6410, Application US/09749280B
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Leach, Martin
; TITLE OF INVENTION: Nucleic Acids Containing Single
; FILE REFERENCE: 15966-610
; CURRENT APPLICATION NUMBER: US/09/749,280B
; CURRENT FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: 60/173,419
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 10038
; SOFTWARE: CuraGen Patent Formatter Version 0.9
; SEQ ID NO 6410
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: (26)...(0)
; OTHER INFORMATION: single nucleotide polymorphism
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Accession number cg42532030
US-09-749-280B-6410

Query Match
Best Local Similarity 64.7%; Score 22.2; DB 5; Length 51;
Best Local Similarity 64.7%; Pred. No. 6.7e+04;
Matches 33; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1184 TTATGTGTCAGAGATGTGGCAGAGCTTTAGCCTGAGCTCAACCTCAT 1234
DB 1 TTATTAATGTGATGAGTGTGGGAAACCTTCAGTACGAGCTCAGATCTTAT 51

RESULT 41
US-60-427-808-134357
; Sequence 134357, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 134357
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-134357

Query Match
Best Local Similarity 92.0%; Score 21.8; DB 11; Length 25;
Best Local Similarity 92.0%; Pred. No. 6.3e+04;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2146 ACTTCATCAGACACGAGGAGCACA 2170
DB 1 ACTTCATCAGACACGAGGAGCACA 25

RESULT 42
US-60-427-836-480873

; Sequence 480873, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 480873
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-480873

Query Match
Best Local Similarity 92.0%; Score 21.8; DB 11; Length 25;
Best Local Similarity 92.0%; Pred. No. 6.3e+04;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 236 GTACTTCACCCAGAGAGAGTGAGG 260
DB 1 GTACTTCACCCAGAGAGAGTGAGG 25

RESULT 43
US-60-449-155-517
; Sequence 517, Application US/60449155
; GENERAL INFORMATION:
; APPLICANT: Keith, Tim
; TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES
; FILE REFERENCE: HUM02-11P
; CURRENT APPLICATION NUMBER: US/60/449,155
; CURRENT FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 1000
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 517
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Human
US-60-449-155-517

Query Match
Best Local Similarity 70.7%; Score 21.8; DB 11; Length 41;
Best Local Similarity 70.7%; Pred. No. 7.9e+04;
Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1348 AGCCTTACATTTGCAGGGAGTGTGAGCAAGCCTTAGCCAG 1388
DB 1 AACCTTATCAGTGCACAGATGTGAGAAAGCCTTCACACAG 41

RESULT 44
PCT-US03-11497-11
; Sequence 11, Application PC/TUS0311497
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies, Inc
; TITLE OF INVENTION: TISSUE SPECIFIC GENES AND GENE CLUSTERS
; FILE REFERENCE: 160 200 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/11497
; CURRENT FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: US 60/372,669
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/411,882
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/424,336
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/374,823
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/376,558
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: US 60/381,366
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 60/403,648

```

:
: PROR FILING DATE: 2002-08-16
:
: NUMBER OF SEQ ID NOS: 344
:
: SOFTWARE: PatentIn version 3.1.1
:
: SEQ ID NO 11
:
: LENGTH: 50
:
: TYPE: DNA
:
: ORGANISM: Homo sapiens
:
PCT-US03-11497-11

```

Query Match	0.88;	Score 21.8;	DB 1;	Length 50;
Best Local Similarity	65.38;	Pred. No. 8	6e+04;	
Matches 32;	Conservative 0;	Mismatches 17;	Indels 0;	Gaps 0

```

Oy 180 CTCATTAGACACCAGAGGACACATTTCAGAGAGAGAGCCTTATATTTGCA 2028
    ||| ||||| | ||| ||| ||| | ||| ||| ||| |||
Db 2 CTCCTTAGATAAAAAAGGCCAGATTATTAAGAACCCTGATTTAATCA 50

```

RESULT 45
US-10-257-848-81/c
; Sequence 81, Application US/10257848
GENERAL INFORMATION:

```

APPLICANT: ITOH, Yasuaki
APPLICANT: SUZUKI, Nobuhiko
APPLICANT: NISHI, Kazumori
APPLICANT: KIZAWA, Hideaki
APPLICANT: HARADA, Masataka
APPLICANT: OGI, Kazuhiko
TITLE OF INVENTION: Novel Insulin/IGF/Relaxin Family Polypeptide and Its DNA
FILE REFERENCE: 2717 USOP
CURRENT APPLICATION NUMBER: US/10/257, 848
CURRENT FILING DATE: 2002-10-17
PRIORITY APPLICATION NUMBER: PCT/JP01/03399
PRIORITY FILING DATE: 2001-04-20
PRIORITY APPLICATION NUMBER: JP 12-126340
PRIORITY FILING DATE: 2000-04-21
PRIORITY APPLICATION NUMBER: JP 12-205587
PRIORITY FILING DATE: 2000-07-03
PRIORITY APPLICATION NUMBER: JP 12-247962
PRIORITY FILING DATE: 2000-08-10
PRIORITY APPLICATION NUMBER: JP 12-395050
PRIORITY FILING DATE: 2000-12-22
NUMBER OF SEQ ID NOS: 86
SEQ ID NO 81
LENGTH: 60
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: for peptide
US-10-257-848-81

```

[illegible]

RESULT 46
US-10-325-899-4332/C
Sequence 4332, Application US/10325899
GENERAL INFORMATION:
APPLICANT: Wohlgenuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Ly, Ngoc
APPLICANT: Woodward, Robert
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING TRANSPLANT
TITLE OF INVENTION: REJECTION
FILE REFERENCE: 506612000122
CURRENT APPLICATION NUMBER: US/10/325,899
CURRENT FILING DATE: 2002-12-20

```

? PRIOR APPLICATION NUMBER: US 60/296,764
? PRIOR FILING DATE: 2001-06-08
? PRIOR APPLICATION NUMBER: US 10/006,290
? PRIOR FILING DATE: 2001-10-22
? PRIOR APPLICATION NUMBER: US 10/131,833
? PRIOR FILING DATE: 2002-04-24
? NUMBER OF SEQ. ID NOS: 9966
? SOFTWARE: PatentIn version 3.1
? SEQ. ID NO 4332
? LENGTH: 50
? TYPE: DNA
? ORGANISM: Homo sapiens
US-10-325-899-4332

```

Query Match	0.88;	Score	21.6;	DB	9;	Length	50;
Best Local Similarity	75.0%;	Pred. No.	9.9e+04;				
Matches	27;	Conservative	0;	Mismatches	9;	Indels	0;
						Gaps	0

QY 888 TCAACCTCTCTTAGCCTCCGAGAGACACAACACTGGG 923
 Db 47 TTAACATCCCTAGCCCTAACCAAGGCACAAACAGGG 12

```

RESULT 47
US-09-749-280B-5462/C
? Sequence 5462, Application US/09749280B
? GENERAL INFORMATION:
? APPLICANT: Shimkets, Richard A.
? APPLICANT: Leach, Martin
? TITLE OF INVENTION: Nucleic Acids Containing Single
? TITLE OF INVENTION: Nucleotide Polymorphisms and Methods of Use Thereof
? FILE REFERENCE: 15966-610
? CURRENT APPLICATION NUMBER: US/09/749,280B
? CURRENT FILING DATE: 2000-12-27
? PRIOR APPLICATION NUMBER: 60/173,419
? PRIOR FILING DATE: 1999-12-28
? NUMBER OF SEQ ID NOS: 10038
? SOFTWARE: Curagen Patent Formatter Version 0.9
? SEQ ID NO 5462
? LENGTH: 50

```

```

? ORGANISM: Homo sapiens
?
? FEATURE:
? NAME/KEY: allele
? LOCATION: (26)..(0)
? OTHER INFORMATION: single nucleotide polymorphism
?
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (25)..(26)
? OTHER INFORMATION: Nucleotide deleted between bases 25 and 26
?
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (0)..(0)
? OTHER INFORMATION: Accession number CG44911411
US-09-749-280B-5462

```

Query Match	0.88;	Score 21.4;	DB 5;	Length 50;
Best Local Similarity	71.88;	Pred. No. 1.1e+05;		
Matches	28;	Conservative	0;	Mismatches 11;
				Indels 0;
				Gaps 0

```

QY      1522  ATGTCGACCTGGAGAGCGGGCAGTCCCTTACCGCGAAGT 1560
          | | | | | | | | | | | | | | | | | | | |
Db      50   AGCACTGCCTGAGATTGGGGCAGGGCTAGACCCGGAAGT 12

RESULT 48
US-10-325-899-4844/C
: Sequence 4844, Application US/10325899
: GENERAL INFORMATION:
: APPLICANT: Mohlgenmuth, Jay
: APPLICANT: Fry, Kirk
: APPLICANT: Ly, Ngoc
: APPLICANT: Woodward, Robert

```

```

OY      1522  ATGTCGCGCTGGAGTGGCGGACGTCCTTAGCGTCAAGT 1560
          | | | | | | | | | | | | | | | | | | | | | |
Db      50   AGCACTGCGCTGGATTTTGGGGCAGCGGTAGACCCGGAAGT 12

RESULT 48
US-10-325-899-4844/C
; Sequence 4844, Application US/10325899
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Ly, Ngoc
; APPLICANT: Woodward, Robert

```

```

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING TRANSPLANT
; FILE REFERENCE: 506612000122
; CURRENT APPLICATION NUMBER: US/10/325, 899.
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 9966
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4844
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-325-899-4844
```

```

Query Match          0.8%; Score 21.4; DB 9; Length 50;
Best Local Similarity 71.8%; Pred. No. 1.1e+05;
Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
```

```

QY      2632 AGCCCATAAAGACCCAGACTGCTGAGTGAGAGAG 2670
DB      39 AACCAAAACATCAGACAGACTCAGCAGCAGTGGGAGGC 1
```

```

RESULT 49
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; Sequence 1151, Application US/09749280B
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: Nucleic Acids Containing Single
; FILE REFERENCE: 15966-610
; CURRENT APPLICATION NUMBER: US/09/749,280B
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: 60/173,419
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 10038
; SOFTWARE: Curagen Patent Formatter Version 0.9
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; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: (26)...(0)
; OTHER INFORMATION: single nucleotide polymorphism
; NAME/KEY: misc_feature
; LOCATION: (25)...(26)
; OTHER INFORMATION: Nucleotide deleted between bases 25 and 26
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; OTHER INFORMATION: Accession number c942924171
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Best Local Similarity 76.5%; Pred. No. 1.3e+05;
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DB      34 AAATGCTTCCAGGCTCTCTGAGAGCCAGAGC 1
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RESULT 50
US-10-089-560-10/c
; Sequence 10, Application us/10089560
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; GENERAL INFORMATION:
; APPLICANT: Straume, Tore
; APPLICANT: Liu, Gang
; TITLE OF INVENTION: Particle Analysis Assay for Biomolecular Quantification
; FILE REFERENCE: 1321.2.71
; CURRENT APPLICATION NUMBER: US/10/089,560
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/158,664
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
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; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Synthetic oligonucleotide
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Query Match          0.8%; Score 21.2; DB 8; Length 50;
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Search completed: June 4, 2003, 12:40:27
Job time : 1950 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 4, 2003, 09:21:00 ; Search time 6053 Seconds
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Title: US-09-898-556A-3
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Gapop 10.0, Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

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4	51	1.8	51	61	US-60-172-373-18031 Sequence 18031, A
5	51	1.8	51	61	US-60-172-373-18032 Sequence 18032, A
6	49.4	1.8	51	61	US-09-718-321A-465 Sequence 465, App
7	49.4	1.8	51	28	US-09-718-321A-869 Sequence 869, App
8	49.4	1.8	51	61	US-60-172-373-18033 Sequence 18033, A
9	49.4	1.8	51	71	US-60-278-258-5294 Sequence 5294, Ap
10	49.4	1.8	51	71	US-60-278-258-5296 Sequence 5296, Ap
11	49.4	1.8	51	71	US-60-278-258-5297 Sequence 5297, Ap
12	49.4	1.8	51	76	US-60-324-185-24475 Sequence 24475, A
13	47.8	1.7	51	76	US-60-278-258-5295 Sequence 5295, Ap
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15	40.4	1.5	51	65	US-60-324-185-4223 Sequence 4223, Ap
16	39.8	1.4	51	65	US-60-213-359-20 Sequence 20, Appl
17	38.2	1.4	51	67	US-60-234-690-1769 Sequence 1769, Ap
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20	35	1.3	51	65	US-60-213-359-2531 Sequence 2531, Ap
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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175	26.6	1.0	56	39	US-10-057-408-49	Sequence 49, Appl	248	25.2	0.9	60	34	US-09-908-975-6302	Sequence 6302, Ap
176	26.4	1.0	51	29	US-09-755-374A-14112	Sequence 14112, A	249	25.2	0.9	60	34	US-09-908-975-18186	Sequence 18186, A
177	26.4	1.0	51	76	US-60-324-185-4165	Sequence 4165, Ap	250	25.2	0.9	60	34	US-09-908-975A-6302	Sequence 6302, Ap
178	26.2	0.9	51	28	US-09-726-173A-6933	Sequence 6933, Ap	251	25.2	0.9	60	34	US-09-908-975A-6302	Sequence 6302, Ap
179	26.2	0.9	51	29	US-09-755-374A-24992	Sequence 24992, A	252	25.2	0.9	60	72	US-60-287-724-6302	Sequence 6302, Ap
180	26.2	0.9	51	65	US-60-213-360-2984	Sequence 2984, Ap	253	25.2	0.9	60	72	US-60-287-724-6302	Sequence 6302, Ap
181	26.2	0.9	51	69	US-60-250-830-1026	Sequence 1026, Ap	254	25	0.9	25	1	PCT-US02-21090-6	Sequence 6, Appl
182	26.2	0.9	51	69	US-60-250-830-1040	Sequence 1040, Ap	255	25	0.9	25	33	US-09-898-556A-6	Sequence 6, Appl
183	26.2	0.9	51	76	US-60-323-966-1026	Sequence 1026, Ap	256	25	0.9	51	61	US-60-172-373-17881	Sequence 17881, A
184	26.2	0.9	51	76	US-60-323-966-1040	Sequence 1040, Ap	257	25	0.9	51	61	US-60-213-360-2804	Sequence 2804, Ap
185	26	0.9	51	29	US-09-726-173A-5033	Sequence 5033, Ap	258	25	0.9	51	65	US-60-213-360-2876	Sequence 2876, Ap
186	26	0.9	51	29	US-09-755-374A-14114	Sequence 14114, A	259	25	0.9	51	65	US-60-213-360-2947	Sequence 2947, Ap
187	26	0.9	51	29	US-09-755-374A-24433	Sequence 24433, A	260	25	0.9	51	65	US-60-213-360-2953	Sequence 2953, Ap
188	26	0.9	51	29	US-09-755-374A-24434	Sequence 24434, A	261	25	0.9	51	65	US-60-213-360-3133	Sequence 3133, Ap
189	26	0.9	51	61	US-60-172-360-29463	Sequence 29463, A	262	25	0.9	51	65	US-60-213-360-3179	Sequence 3179, Ap
190	26	0.9	51	65	US-60-213-360-2802	Sequence 2802, Ap	263	25	0.9	51	69	US-60-250-830-1080	Sequence 1080, Ap
191	26	0.9	51	76	US-60-324-185-3925	Sequence 3925, Ap	264	25	0.9	51	71	US-60-278-258-5756	Sequence 5756, Ap
192	25.8	0.9	51	29	US-09-755-374A-14107	Sequence 14107, A	265	25	0.9	51	71	US-60-278-258-5803	Sequence 5803, Ap
193	25.8	0.9	51	65	US-60-213-359-420	Sequence 420, App	266	25	0.9	51	76	US-60-323-966-1080	Sequence 1080, Ap
194	25.8	0.9	51	65	US-60-213-360-2755	Sequence 2755, Ap	267	25	0.9	51	76	US-60-324-185-4179	Sequence 4179, Ap
195	25.8	0.9	51	71	US-60-278-258-5870	Sequence 5870, Ap	268	25	0.9	51	76	US-60-324-185-4561	Sequence 4561, Ap
196	25.8	0.9	51	76	US-60-324-185-3953	Sequence 3953, Ap	269	25	0.9	51	76	US-60-324-185-4587	Sequence 4587, Ap
197	25.8	0.9	51	76	US-60-324-185-4104	Sequence 4104, Ap	270	25	0.9	51	76	US-60-324-185-45803	Sequence 45803, A
198	25.8	0.9	51	76	US-60-324-185-4178	Sequence 4178, Ap	271	24.8	0.9	51	71	US-60-278-258-3590	Sequence 3590, Ap
199	25.8	0.9	60	39	US-10-057-408-45	Sequence 45, Appl	272	24.8	0.9	51	71	US-60-278-258-5843	Sequence 5843, Ap
200	25.6	0.9	51	65	US-60-213-359-311	Sequence 311, App	273	24.8	0.9	51	71	US-60-278-258-13326	Sequence 13326, A
201	25.6	0.9	51	65	US-60-213-360-2766	Sequence 2766, Ap	274	24.8	0.9	60	34	US-09-908-975-6660	Sequence 6660, Ap
202	25.6	0.9	51	65	US-60-213-360-2822	Sequence 2822, Ap	275	24.8	0.9	60	34	US-09-908-975-6664	Sequence 6664, Ap
203	25.6	0.9	51	69	US-60-250-830-956	Sequence 956, App	276	24.8	0.9	60	34	US-09-908-975-6859	Sequence 6859, Ap
204	25.6	0.9	51	69	US-60-250-830-1022	Sequence 1022, Ap	277	24.8	0.9	60	34	US-09-908-975A-6660	Sequence 6660, Ap
205	25.6	0.9	51	69	US-60-250-830-1048	Sequence 1048, Ap	278	24.8	0.9	60	34	US-09-908-975A-6664	Sequence 6664, Ap
206	25.6	0.9	51	71	US-60-278-258-5767	Sequence 5767, Ap	279	24.8	0.9	60	34	US-09-908-975A-6859	Sequence 6859, Ap
207	25.6	0.9	51	71	US-60-278-258-5781	Sequence 5781, Ap	280	24.8	0.9	60	72	US-60-287-724-6660	Sequence 6660, Ap
208	25.6	0.9	51	71	US-60-278-258-5797	Sequence 5797, Ap	281	24.8	0.9	60	72	US-60-287-724-6664	Sequence 6664, Ap
209	25.6	0.9	51	71	US-60-278-258-6273	Sequence 6273, Ap	282	24.8	0.9	60	72	US-60-287-724-6859	Sequence 6859, Ap
210	25.6	0.9	51	76	US-60-323-966-956	Sequence 956, App	283	24.6	0.9	51	29	US-09-755-374A-27475	Sequence 27475, A
211	25.6	0.9	51	76	US-60-323-966-1022	Sequence 1022, Ap	284	24.6	0.9	51	29	US-09-755-374A-27476	Sequence 27476, A
212	25.6	0.9	51	76	US-60-323-966-1048	Sequence 1048, Ap	285	24.6	0.9	51	61	US-60-172-373-17948	Sequence 17948, A
213	25.6	0.9	51	76	US-60-324-185-3608	Sequence 3608, Ap	286	24.6	0.9	51	61	US-60-172-373-17973	Sequence 17973, A
214	25.6	0.9	51	76	US-60-324-185-3787	Sequence 3787, Ap	287	24.6	0.9	51	65	US-60-213-359-118	Sequence 118, App
215	25.6	0.9	51	76	US-60-324-185-4544	Sequence 4544, Ap	288	24.6	0.9	51	65	US-60-213-360-2910	Sequence 2910, Ap
216	25.6	0.9	51	76	US-60-324-185-11021	Sequence 11021, A	289	24.6	0.9	51	69	US-60-250-830-1032	Sequence 1032, Ap
217	25.6	0.9	51	76	US-60-324-185-32332	Sequence 32332, A	290	24.6	0.9	51	71	US-60-278-232-8634	Sequence 8634, Ap
218	25.6	0.9	56	39	US-10-057-408-40	Sequence 40, Appl	291	24.6	0.9	51	76	US-60-323-966-1032	Sequence 1032, Ap
219	25.6	0.9	60	34	US-09-908-975-6829	Sequence 6829, Ap	292	24.6	0.9	51	76	US-60-324-185-4102	Sequence 4102, Ap
220	25.6	0.9	60	34	US-09-908-975A-6829	Sequence 6829, Ap	293	24.6	0.9	51	76	US-60-324-185-4102	Sequence 4102, Ap
221	25.6	0.9	60	72	US-60-287-724-6829	Sequence 6829, Ap	294	24.6	0.9	51	76	US-60-324-185-4518	Sequence 4518, Ap
222	25.4	0.9	51	61	US-60-172-373-5407	Sequence 5407, Ap	295	24.6	0.9	51	76	US-60-324-185-4528	Sequence 4528, Ap
223	25.4	0.9	51	61	US-60-172-373-17769	Sequence 17769, A	296	24.6	0.9	51	76	US-60-324-185-14693	Sequence 14693, A
224	25.4	0.9	51	65	US-60-213-360-2778	Sequence 2778, Ap	297	24.6	0.9	55	39	US-10-057-408-50	Sequence 50, Appl
225	25.4	0.9	51	65	US-60-213-360-2825	Sequence 2825, Ap	298	24.6	0.9	60	34	US-09-908-975-6759	Sequence 6759, Ap
226	25.4	0.9	51	71	US-60-278-232-1474	Sequence 1474, Ap	299	24.6	0.9	60	34	US-09-908-975A-6759	Sequence 6759, Ap
227	25.4	0.9	51	71	US-60-278-258-5696	Sequence 5696, Ap	300	24.6	0.9	60	72	US-60-287-724-6759	Sequence 6759, Ap
228	25.4	0.9	51	71	US-60-278-258-5799	Sequence 5799, Ap	301	24.4	0.9	51	29	US-09-755-374A-14113	Sequence 14113, A
229	25.4	0.9	51	71	US-60-278-258-5824	Sequence 5824, Ap	302	24.4	0.9	51	61	US-60-172-373-17867	Sequence 17867, A
230	25.4	0.9	51	76	US-60-324-185-3937	Sequence 3937, Ap	303	24.4	0.9	51	65	US-60-213-359-156	Sequence 156, App
231	25.4	0.9	51	76	US-60-324-185-3977	Sequence 3977, Ap	304	24.4	0.9	51	71	US-60-278-258-5754	Sequence 5754, Ap
232	25.4	0.9	51	76	US-60-324-185-4251	Sequence 4251, Ap	305	24.4	0.9	51	71	US-60-278-258-5779	Sequence 5779, Ap
233	25.4	0.9	51	76	US-60-324-185-10763	Sequence 30763, A	306	24.4	0.9	51	76	US-60-324-185-1123	Sequence 4413, Ap
234	25.4	0.9	60	34	US-09-908-975-7136	Sequence 7136, Ap	307	24.4	0.9	51	76	US-60-324-185-1413	Sequence 4413, Ap
235	25.4	0.9	60	34	US-09-908-975A-7136	Sequence 7136, Ap	308	24.4	0.9	51	76	US-60-324-185-1413	Sequence 4413, Ap
236	25.4	0.9	60	72	US-60-287-724-7136	Sequence 7136, Ap	309	24.4	0.9	51	76	US-60-324-185-10998	Sequence 10998, A
237	25.2	0.9	50	1	PCT-US01-47856-2511	Sequence 2511, Ap	310	24.4	0.9	60	34	US-60-324-185-10845	Sequence 30845, A
238	25.2	0.9	50	1	PCT-US01-47856-3660	Sequence 3660, Ap	311	24.4	0.9	60	34	US-09-908-975-6321	Sequence 6321, Ap
239	25.2	0.9	50	40	US-10-131-827-2511	Sequence 2511, Ap	312	24.4	0.9	60	34	US-09-908-975A-6321	Sequence 6321, Ap
240	25.2	0.9	50	40	US-10-131-827-3660	Sequence 3660, Ap	313	24.4	0.9	60	34	US-09-908-975A-6790	Sequence 6790, Ap

314	24.4	0.9	60	72	US-60-287-724-6321	Sequence 6321, Ap	C 387	23.2	0.8	50	12	US-08-810-325-2558	Sequence 2558, Ap
315	24.4	0.9	60	72	US-60-287-724-6390	Sequence 6790, Ap	C 388	23.2	0.8	50	29	US-60-012-458-35	Sequence 35, Appl
316	24.2	0.9	51	61	US-60-172-373-5406	Sequence 5406, Ap	C 389	23.2	0.8	51	45	US-09-755-374A-249	Sequence 249, App
317	24.2	0.9	51	61	US-60-172-373-12209	Sequence 12209, A	C 390	23.2	0.8	51	29	US-09-755-374A-250	Sequence 250, App
318	24.2	0.9	51	71	US-60-278-232-1466	Sequence 1466, Ap	C 391	23.2	0.8	51	61	US-60-212-373-5568	Sequence 5568, Ap
319	24.2	0.9	51	71	US-60-278-258-15070	Sequence 15070, A	C 392	23.2	0.8	51	61	US-60-172-373-5685	Sequence 5685, Ap
320	24.2	0.9	51	76	US-60-324-185-3766	Sequence 3766, Ap	C 393	23.2	0.8	51	65	US-60-324-185-3095	Sequence 3095, Ap
321	24	0.9	51	29	US-09-755-374A-5299	Sequence 5299, Ap	C 394	23.2	0.8	60	34	US-09-908-975-6404	Sequence 6404, Ap
322	24	0.9	51	29	US-60-213-359-580	Sequence 580, App	C 395	23.2	0.8	60	34	US-09-908-975A-6404	Sequence 6404, Ap
323	24	0.9	51	65	US-60-213-360-8845	Sequence 2845, Ap	C 396	23.2	0.8	60	72	US-60-287-724-6404	Sequence 6404, Ap
324	24	0.9	51	69	US-60-250-830-1017	Sequence 1017, Ap	C 397	23	0.8	51	29	US-09-726-173A-2987	Sequence 2987, Ap
325	24	0.9	51	71	US-60-278-232-6547	Sequence 6547, Ap	C 398	23	0.8	51	29	US-09-755-374A-27917	Sequence 27917, A
326	24	0.9	51	76	US-60-323-966-1017	Sequence 1017, Ap	C 399	23	0.8	51	61	US-60-172-373-733	Sequence 733, App
327	24	0.9	51	76	US-60-324-185-4050	Sequence 4050, Ap	C 400	23	0.8	51	61	US-60-172-373-24751	Sequence 24751, A
328	24	0.9	51	76	US-60-324-185-11000	Sequence 11000, A	C 401	23	0.8	51	65	US-60-213-360-2937	Sequence 2937, Ap
329	24	0.9	51	76	US-60-324-185-14093	Sequence 14093, A	C 402	23	0.8	51	71	US-60-278-258-6698	Sequence 5698, Ap
C 330	24	0.9	58	30	US-09-775-049-14	Sequence 14, Appl	C 403	23	0.8	51	71	US-60-278-258-5763	Sequence 5763, Ap
C 331	23.8	0.9	51	29	US-09-726-173A-6713	Sequence 6713, Ap	C 404	23	0.8	51	71	US-60-278-258-5879	Sequence 5879, Ap
332	23.8	0.9	51	29	US-09-755-374A-24357	Sequence 24357, A	C 405	23	0.8	51	71	US-60-278-258-5879	Sequence 5879, Ap
333	23.8	0.9	51	29	US-09-755-374A-24358	Sequence 24358, A	C 406	23	0.8	51	76	US-60-324-185-3678	Sequence 3678, Ap
334	23.8	0.9	51	61	US-60-172-373-5343	Sequence 5343, Ap	C 407	23	0.8	51	76	US-09-912-293-732	Sequence 732, App
335	23.8	0.9	51	61	US-60-172-373-5652	Sequence 5652, Ap	C 408	23	0.8	51	76	US-09-908-975A-6323	Sequence 6323, Ap
336	23.8	0.9	51	61	US-60-172-373-5675	Sequence 5675, Ap	C 409	23	0.8	59	24	US-09-628-860-9	Sequence 9, Appl
337	23.8	0.9	51	61	US-60-172-373-17799	Sequence 17799, A	C 410	23	0.8	60	34	US-09-906-393A-34	Sequence 34, Appl
338	23.8	0.9	51	65	US-60-213-360-3728	Sequence 2728, Ap	C 411	23	0.8	60	34	US-09-908-975A-6323	Sequence 6323, Ap
339	23.8	0.9	51	65	US-60-213-360-2748	Sequence 2748, Ap	C 412	23	0.8	60	72	US-60-287-724-6323	Sequence 6323, Ap
340	23.8	0.9	51	65	US-60-213-360-8824	Sequence 2824, Ap	C 413	22.8	0.8	51	61	US-60-172-373-24959	Sequence 24959, A
341	23.8	0.9	51	65	US-60-213-360-8848	Sequence 2848, Ap	C 414	22.8	0.8	51	65	US-60-213-359-90	Sequence 90, Appl
342	23.8	0.9	51	65	US-60-213-360-9921	Sequence 2921, Ap	C 415	22.8	0.8	51	65	US-60-213-359-326	Sequence 326, App
343	23.8	0.9	51	71	US-60-278-232-10275	Sequence 10275, A	C 416	22.8	0.8	51	65	US-60-213-362-3122	Sequence 3122, App
C 344	23.8	0.9	51	71	US-60-278-258-5783	Sequence 5783, Ap	C 417	22.8	0.8	51	65	US-60-213-362-5466	Sequence 5466, Ap
345	23.8	0.9	51	71	US-60-278-258-5814	Sequence 5814, Ap	C 418	22.8	0.8	51	65	US-60-278-258-5769	Sequence 5769, Ap
346	23.8	0.9	51	71	US-60-278-258-8216	Sequence 8216, Ap	C 419	22.8	0.8	51	76	US-60-324-185-1187	Sequence 1187, Ap
347	23.8	0.9	51	76	US-60-324-185-3672	Sequence 3672, Ap	C 420	22.8	0.8	51	76	US-60-324-185-3614	Sequence 3614, Ap
348	23.8	0.9	51	76	US-60-324-185-9949	Sequence 3949, Ap	C 421	22.8	0.8	51	76	US-60-324-185-14602	Sequence 14602, A
349	23.8	0.9	51	76	US-60-324-185-4125	Sequence 4125, Ap	C 422	22.8	0.8	51	76	US-60-324-185-14682	Sequence 14682, A
350	23.8	0.9	51	76	US-60-324-185-4250	Sequence 4250, Ap	C 423	22.8	0.8	51	76	US-60-324-185-31882	Sequence 31882, A
351	23.8	0.9	51	76	US-60-324-185-4255	Sequence 4255, Ap	C 424	22.8	0.8	60	20	US-09-535-897-16793	Sequence 16793, A
352	23.8	0.9	51	76	US-60-324-185-4371	Sequence 4371, Ap	C 425	22.8	0.8	60	34	US-09-908-975A-16334	Sequence 16334, A
C 353	23.8	0.9	51	76	US-60-324-185-8933	Sequence 8933, Ap	C 426	22.8	0.8	60	34	US-09-908-975A-23585	Sequence 23585, A
C 354	23.8	0.9	55	39	US-10-057-408-41	Sequence 41, Appl	C 427	22.8	0.8	60	34	US-09-908-975A-16334	Sequence 16334, A
C 355	23.8	0.9	60	34	US-09-908-975-6437	Sequence 6437, Ap	C 428	22.8	0.8	60	34	US-09-908-975A-23585	Sequence 23585, A
356	23.8	0.9	60	34	US-09-908-975-6557	Sequence 6557, Ap	C 429	22.8	0.8	60	72	US-60-287-724-16334	Sequence 16334, A
357	23.8	0.9	60	34	US-09-908-975-15198	Sequence 15198, A	C 430	22.8	0.8	60	72	US-60-287-724-23585	Sequence 23585, A
358	23.8	0.9	60	34	US-09-908-975A-6437	Sequence 6437, Ap	C 431	22.6	0.8	51	71	US-60-278-232-1030	Sequence 1030, Ap
359	23.8	0.9	60	34	US-09-908-975A-6557	Sequence 6557, Ap	C 432	22.6	0.8	51	71	US-60-278-232-8741	Sequence 8741, Ap
360	23.8	0.9	60	34	US-09-908-975A-15198	Sequence 15198, A	C 433	22.6	0.8	51	76	US-60-324-185-3647	Sequence 3647, Ap
361	23.8	0.9	60	72	US-60-287-724-6437	Sequence 6437, Ap	C 434	22.6	0.8	60	34	US-09-908-975A-6392	Sequence 6392, Ap
362	23.8	0.9	60	72	US-60-287-724-6557	Sequence 6557, Ap	C 435	22.6	0.8	60	34	US-09-908-975A-6392	Sequence 6392, Ap
C 363	23.8	0.9	60	72	US-60-287-724-15198	Sequence 15198, A	C 436	22.6	0.8	60	34	US-09-908-975A-6392	Sequence 6392, Ap
C 364	23.6	0.9	51	61	US-60-172-360-10854	Sequence 10854, A	C 437	22.6	0.8	60	72	US-60-287-724-6392	Sequence 6392, Ap
365	23.6	0.9	51	65	US-60-213-359-2526	Sequence 2526, Ap	C 438	22.4	0.8	44	69	US-60-253-378-11078	Sequence 11078
366	23.6	0.9	51	65	US-60-213-360-2744	Sequence 2744, Ap	C 439	22.4	0.8	51	61	US-60-172-360-7702	Sequence 7702, Ap
367	23.6	0.9	51	65	US-60-213-360-2813	Sequence 2813, Ap	C 440	22.4	0.8	51	61	US-60-172-373-17873	Sequence 17873, A
368	23.6	0.9	51	71	US-60-278-258-5758	Sequence 5758, Ap	C 441	22.4	0.8	51	71	US-60-278-258-5695	Sequence 5695, Ap
369	23.6	0.9	51	71	US-60-278-258-5875	Sequence 5875, Ap	C 442	22.4	0.8	51	71	US-60-278-258-5839	Sequence 5839, Ap
370	23.6	0.9	51	76	US-60-324-185-3927	Sequence 3927, Ap	C 443	22.4	0.8	51	76	US-60-324-185-4257	Sequence 4257, Ap
371	23.6	0.9	51	76	US-60-324-185-4036	Sequence 4036, Ap	C 444	22.4	0.8	54	39	US-60-324-185-4898	Sequence 4898, Ap
372	23.6	0.9	55	34	US-09-912-292-35603	Sequence 35603, A	C 445	22.4	0.8	54	39	US-10-055-711-32	Sequence 32, Appl
C 373	23.4	0.8	51	61	US-60-172-360-14666	Sequence 14666, A	C 446	22.4	0.8	60	34	US-09-908-975A-16416	Sequence 16416, A
374	23.4	0.8	51	61	US-60-172-360-21384	Sequence 21384, A	C 447	22.4	0.8	60	34	US-09-908-975A-16416	Sequence 16416, A
375	23.4	0.8	51	61	US-60-172-377-6853	Sequence 6853, Ap	C 448	22.4	0.8	60	34	US-09-908-975A-16416	Sequence 16416, A
376	23.4	0.8	51	65	US-60-213-360-2818	Sequence 2818, Ap	C 449	22.4	0.8	60	39	US-10-057-408-39	Sequence 39, Appl
377	23.4	0.8	51	71	US-60-278-258-5874	Sequence 5874, Ap	C 450	22.4	0.8	60	39	US-10-057-408-48	Sequence 48, Appl
378	23.4	0.8	51	71	US-60-278-258-5887	Sequence 5887, Ap	C 451	22.4	0.8	60	39	US-09-912-263-182	Sequence 182, App
379	23.4	0.8	51	76	US-60-324-185-3663	Sequence 3663, Ap	C 452	22.4	0.8	47	65	US-09-114-053-1088	Sequence 1088, Ap
380	23.4	0.8	51	76	US-60-324-185-4220	Sequence 4220, Ap	C 453	22.2	0.8	50	15	US-09-420-691-4261	Sequence 4261, Ap
381	23.4	0.8	51	76	US-60-324-185-10995	Sequence 10995, A	C 454	22.2	0.8	51	29	US-09-726-173A-6714	Sequence 6714, Ap
C 382	23.4	0.8	51	76	US-60-324-185-30557	Sequence 30557, A	C 455	22.2	0.8	51	29	US-60-172-360-29241	Sequence 29241, A
C 383	23.4	0.8	60	34	US-09-908-975A-17236	Sequence 17236, A	C 456	22.2	0.8	61	61	US-60-172-373-17903	Sequence 17903, A
C 384	23.4	0.8	60	34	US-09-908-975A-17236	Sequence 17236, A	C 457	22.2	0.8				
C 385	23.4	0.8	60	72	US-60-287-724-17236	Sequence 17236, A	C 458	22.2	0.8				
386	23.2	0.8	47	65	US-60-216-745-2667	Sequence 2667, Ap	C 459	22.2	0.8				

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460 22.2 0.8 51 61 US-60-172-377-10606 Sequence 10606, A
461 22.2 0.8 51 65 US-60-213-360-2725 Sequence 2725, Ap
462 22.2 0.8 51 65 US-60-213-360-2726 Sequence 2726, Ap
463 22.2 0.8 51 65 US-60-213-360-2790 Sequence 2790, Ap
464 22.2 0.8 51 65 US-60-213-360-2905 Sequence 2905, Ap
465 22.2 0.8 51 65 US-60-213-360-2912 Sequence 2912, Ap
466 22.2 0.8 51 65 US-60-213-360-2913 Sequence 2913, Ap
467 22.2 0.8 51 65 US-60-213-360-2958 Sequence 2958, Ap
468 22.2 0.8 51 69 US-60-250-830-816 Sequence 816, App
469 22.2 0.8 51 69 US-60-250-830-947 Sequence 947, App
470 22.2 0.8 51 69 US-60-250-830-1005 Sequence 1005, Ap
471 22.2 0.8 51 69 US-60-250-830-1006 Sequence 1006, Ap
472 22.2 0.8 51 69 US-60-250-830-1045 Sequence 1045, Ap
473 22.2 0.8 51 71 US-60-278-232-10137 Sequence 10137, A
474 22.2 0.8 51 71 US-60-278-258-5992 Sequence 5992, Ap
475 22.2 0.8 51 71 US-60-278-561-11075 Sequence 11075, A
476 22.2 0.8 51 76 US-60-323-966-816 Sequence 816, App
477 22.2 0.8 51 76 US-60-323-966-947 Sequence 947, App
478 22.2 0.8 51 76 US-60-323-966-1005 Sequence 1005, Ap
479 22.2 0.8 51 76 US-60-323-966-1006 Sequence 1006, Ap
480 22.2 0.8 51 76 US-60-323-966-1045 Sequence 1045, Ap
481 22.2 0.8 51 76 US-60-324-185-3617 Sequence 3617, Ap
482 22.2 0.8 51 76 US-60-324-185-14797 Sequence 14797, A
483 22.2 0.8 60 24 US-09-635-644-11062 Sequence 11062, A
484 22.2 0.8 60 34 US-09-908-975-5840 Sequence 5840, Ap
485 22.2 0.8 60 34 US-09-908-975-5877 Sequence 5877, Ap
486 22.2 0.8 60 34 US-09-908-975-5877 Sequence 5877, Ap
487 22.2 0.8 60 34 US-09-908-975-8235 Sequence 8235, Ap
488 22.2 0.8 60 34 US-09-908-975A-5840 Sequence 5840, Ap
489 22.2 0.8 60 34 US-09-908-975A-5877 Sequence 5877, Ap
490 22.2 0.8 60 34 US-09-908-975A-6637 Sequence 6637, Ap
491 22.2 0.8 60 34 US-09-908-975A-8235 Sequence 8235, Ap
492 22.2 0.8 60 72 US-60-287-724-5840 Sequence 5840, Ap
493 22.2 0.8 60 72 US-60-287-724-5877 Sequence 5877, Ap
494 22.2 0.8 60 72 US-60-287-724-6637 Sequence 6637, Ap
495 22.2 0.8 60 72 US-60-287-724-8235 Sequence 8235, Ap
496 22.2 0.8 60 69 US-60-253-654-25104 Sequence 25104, A
497 22.2 0.8 40 69 US-60-255-592-25104 Sequence 25104, A
498 22.2 0.8 51 29 US-09-755-374A-13101 Sequence 13101, A
499 22.2 0.8 51 61 US-60-172-360-2006 Sequence 2006, Ap
500 22.2 0.8 51 61 US-60-172-373-18177 Sequence 18177, A
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ALIGNMENTS

RESULT 1

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US-09-908-975-6782
; Sequence 6782, Application US/09908975
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908, 975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6782
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-6782
```

Query Match

2.2%; Score 60; DB 34; Length 60;

Best Local Similarity 100.0%; Pred. No. 3,4e-06; Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1792 GCAGAGGTTGGCAGAGGCTTAACCTGTTAGGCACAGAGGGCAGACTCAGTGCTT 1851
      |||||||
DB 1 GCAGAGGTTGGCAGAGGCTTAACCTGTTAGGCACAGAGGGCAGACTCAGTGCTT 60
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RESULT 2

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US-09-908-975A-6782
; Sequence 6782, Application US/09908975A
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36688-0006
; CURRENT APPLICATION NUMBER: US/09/908, 975A
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6782
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975A-6782
```

Query Match 2.2%; Score 60; DB 34; Length 60;

Best Local Similarity 100.0%; Pred. No. 3,4e-06; Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1792 GCAGAGGTTGGCAGAGGCTTAACCTGTTAGGCACAGAGGGCAGACTCAGTGCTT 1851
      |||||||
DB 1 GCAGAGGTTGGCAGAGGCTTAACCTGTTAGGCACAGAGGGCAGACTCAGTGCTT 60
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RESULT 3

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US-60-287-724-6782
; Sequence 6782, Application US/60287724
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
; FILE REFERENCE: 36688-0004
; CURRENT APPLICATION NUMBER: US/60/287,724
; CURRENT FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6782
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-287-724-6782
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Query Match 2.2%; Score 60; DB 72; Length 60;

Best Local Similarity 100.0%; Pred. No. 3,4e-06; Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1792 GCAGAGGTTGGCAGAGGCTTAACCTGTTAGGCACAGAGGGCAGACTCAGTGCTT 1851
      |||||||
DB 1 GCAGAGGTTGGCAGAGGCTTAACCTGTTAGGCACAGAGGGCAGACTCAGTGCTT 60
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RESULT 4

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; US-60-172-373-18031
; Sequence 18031, Application US/60172373
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: Method for the identification of Sequence Polymorphisms Using
; FILE REFERENCE: Polynucleotide Sequence Databases, and Single Nucleotide Polymor
; FILE REFERENCE: GX-0006 P
; CURRENT APPLICATION NUMBER: US/60/172,373
; CURRENT FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 25,772
; SOFTWARE: PERL Program
; SEQ ID NO 18031
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: SNP00003872
; FEATURE:
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 346325.1, 410, G->T
; US-60-172-373-18031
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Query Match

1.8%; Score 51; DB 61; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.0013;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1629 GGCCTTACCCGGAATCAACCTGTACACGACGAGACACTCAGG 1679
DB 1 GGCCTTACCCGGAATCAACCTGTACACGACGAGACACTCAGG 51
```

RESULT 5

```
; US-60-172-373-18032
; Sequence 18032, Application US/60172373
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: Method for the identification of Sequence Polymorphisms Using
; FILE REFERENCE: Polynucleotide Sequence Databases, and Single Nucleotide Polymor
; FILE REFERENCE: GX-0006 P
; CURRENT APPLICATION NUMBER: US/60/172,373
; CURRENT FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 25,772
; SOFTWARE: PERL Program
; SEQ ID NO 18032
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: SNP00003873
; FEATURE:
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 346325.1, 757, T->C
; US-60-172-373-18032
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Query Match

1.8%; Score 51; DB 61; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.0013;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1974 TCACACCTCATTAACACGACGAGACATTCAGAGAGAGCCTTATATT 2024
DB 1 TCACACCTCATTAACACGACGAGACATTCAGAGAGAGCCTTATATT 51
```

RESULT 6

```
; US-09-718-321A-465/c
; Sequence 465, Application US/09718321A
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Leach, Martin D.
; TITLE OF INVENTION: NUCLEIC ACIDS CONTAINING SINGLE NUCLEIC ACID POLYMORPHISMS AND
; FILE REFERENCE: USE THEREOF
; FILE REFERENCE: 15966-599
; CURRENT APPLICATION NUMBER: US/09/718,321A
; CURRENT FILING DATE: 2002-06-20
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1468
; SOFTWARE: Curagen Patent Formatter Version 0.9
; SEQ ID NO 465
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: (26)...(0)
; OTHER INFORMATION: single nucleotide polymorphism
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Accession number cg43297259
; US-09-718-321A-465
```

Query Match

1.8%; Score 49.4; DB 28; Length 51;
Best Local Similarity 98.0%; Pred. No. 0.0036;

Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 1378 GCTTAGCCAGAGACACACCTCATCAGACCTTAAGACACACAGAG 1428
DB 51 GCTTAGCCAGAGACACACCTCATCAGACCTTAAGACACACAGAG 1
```

RESULT 7

```
; US-09-718-321A-869/c
; Sequence 869, Application US/09718321A
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Leach, Martin D.
; TITLE OF INVENTION: NUCLEIC ACIDS CONTAINING SINGLE NUCLEIC ACID POLYMORPHISMS AND
; FILE REFERENCE: 15966-599
; CURRENT APPLICATION NUMBER: US/09/718,321A
; CURRENT FILING DATE: 2002-06-20
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1468
; SOFTWARE: Curagen Patent Formatter Version 0.9
; SEQ ID NO 869
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: (26)...(0)
; OTHER INFORMATION: single nucleotide polymorphism
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Accession number cg43297259
; US-09-718-321A-869
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Query Match

1.8%; Score 49.4; DB 28; Length 51;
Best Local Similarity 98.0%; Pred. No. 0.0036;

Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 1362 AGGAGGTGTAGCAGAGCCTTAGCCAGAGTCAACCTCATCAGACACTTA 1412
DB 1 AGGAGGTGTAGCAGAGCCTTAGCCAGAGTCAACCTCATCAGACACTTA 1412
```

Db 51 AGGAGTGTAGCAAGGCTTTAGCCGGAAGTCACACCTCATCAGACCTTA 1

RESULT 8

US-60-172-373-18033
; Sequence 18033, Application US/60172373
; GENERAL INFORMATION:
; APPLICANT: Morris, Macdonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymor
; FILE REFERENCE: GX-0006 P
; CURRENT APPLICATION NUMBER: US/60/172,373
; CURRENT FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 25,772
; SOFTWARE: PERL Program
; SEQ ID NO 18033
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID NO: SNP00024175
; FEATURE:
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 346325.1, 615, C->T
US-60-172-373-18033

Query Match

Best Local Similarity 1.8%; Score 49.4; DB 61; Length 51;
Best Local Similarity 98.0%; Pred. No. 0.0036;
Matches 50: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1834 GGGACACTCAGTGCCCTTTGTGTGCGAGGAGTGGCGCAAGGCTTTGTG 1884
Db 1 GGGCACACTCAGTGCCCTTTGTGTGTAAGGAGTGGCGCAAGGCTTTGTG 51

RESULT 9

US-60-278-258-5294
; Sequence 5294, Application US/60278258
; GENERAL INFORMATION:
; APPLICANT: Morris, Macdonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide
; FILE REFERENCE: GX-0010-1 P
; CURRENT APPLICATION NUMBER: US/60/278,258
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 17730
; SOFTWARE: PERL Program
; SEQ ID NO 5294
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID NO: SNP00075163
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 346325.1, 421, T->G
US-60-278-258-5294

Query Match

Best Local Similarity 1.8%; Score 49.4; DB 71; Length 51;
Best Local Similarity 98.0%; Pred. No. 0.0036;
Matches 50: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 643 AGGAGAAAGCTCCAGACTCCTGTTGGGAGAGTAAGCAAAATGGCACTT 693
Db 1 AGGAGAAAGCTCCAGACTCCTGTTGGGAGAGTAAGCAAAATGGCACTT 51

RESULT 10

US-60-278-258-5296
; Sequence 5296, Application US/60278258
; GENERAL INFORMATION:
; APPLICANT: Morris, Macdonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide
; FILE REFERENCE: GX-0010-1 P
; CURRENT APPLICATION NUMBER: US/60/278,258
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 17730
; SOFTWARE: PERL Program
; SEQ ID NO 5296
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID NO: SNP00075165
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 346325.1, 914, A->C
US-60-278-258-5296

Query Match

Best Local Similarity 1.8%; Score 49.4; DB 71; Length 51;
Best Local Similarity 98.0%; Pred. No. 0.0036;
Matches 50: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1136 GAAGTCAGCTCTTTACACATCAAGGAGACACACTCAAGGCTCAAGCCTTA 1186
Db 1 GAAGTCAGCTCTTTACACATCAAGGAGACACACTCAAGGCTCAAGCCTTA 51

RESULT 11

US-60-278-258-5297
; Sequence 5297, Application US/60278258
; GENERAL INFORMATION:
; APPLICANT: Morris, Macdonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide
; FILE REFERENCE: GX-0010-1 P
; CURRENT APPLICATION NUMBER: US/60/278,258
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 17730
; SOFTWARE: PERL Program
; SEQ ID NO 5297
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID NO: SNP00075166
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 346325.1, 2262, C->T
US-60-278-258-5297

Query Match

Best Local Similarity 1.8%; Score 49.4; DB 71; Length 51;
Best Local Similarity 98.0%; Pred. No. 0.0036;
Matches 50: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2483 TTGCTGCTCTTCTCCGATTTGATCCACCTTCACCTATTTACGTATA 2533
Db 1 TTGCTGCTCTTCTCCGATTTGATCCACCTTCACCTATTTACGTATA 51

```
RESULT 12
US-60-324-185-24475
; Sequence 24475, Application US/60324185
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preethi
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; FILE REFERENCE: GX-0019-1 P
; CURRENT APPLICATION NUMBER: US/60/324,185
; CURRENT FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 35862
; SOFTWARE: PERL Program
; SEQ ID NO 24475
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: SNP00115145
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 346325.1, 2091, C->G
US-60-324-185-24475

Query Match
Best Local Similarity 1.8%; Score 49.4; DB 76; Length 51;
Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2060 CACCTTATCAGACATCAGAGACACACTCAGATAGAACTTTATGTGTA 2110
DB 1 CAACCTTATCAGACATCAGAGACACACTCAGATAGAACTTTATGTGTA 51

RESULT 13
US-50-278-258-5295
; Sequence 5295, Application US/60278258
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preethi
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; FILE REFERENCE: GX-0010-1 P
; CURRENT APPLICATION NUMBER: US/60/278,258
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 17730
; SOFTWARE: PERL Program
; SEQ ID NO 5295
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: SNP00075164
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 346325.1, 886, T->G
US-60-278-258-5295

Query Match
Best Local Similarity 1.7%; Score 47.8; DB 71; Length 51;
Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1108 GCAAGATTGTGAGCAGAGCTTTACTTGAAGTCGAACCTCTTACACATC 1158
DB 1 GCAAGATTGTGAGCAGAGCTTTACTTGAAGTCGAACCTCTTACACATC 51
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```
RESULT 14
US-60-324-185-4221
; Sequence 4221, Application US/60324185
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preethi
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; FILE REFERENCE: GX-0019-1 P
; CURRENT APPLICATION NUMBER: US/60/324,185
; CURRENT FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 35862
; SOFTWARE: PERL Program
; SEQ ID NO 4221
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: SNP00106336
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 1082325.11, 1102, C->T
US-60-324-185-4221

Query Match
Best Local Similarity 1.5%; Score 41.4; DB 76; Length 51;
Matches 45; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 994 GCACACACTCTGCGGGAAGCCCTTATGTGTGTCAGAGGATGTGGCGAGCT 1044
DB 1 GCACACACTCTGCGGGAAGCCCTTATGTGTGTCAGAGGATGTGGCGAGCT 51

RESULT 15
US-60-324-185-4223
; Sequence 4223, Application US/60324185
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preethi
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; FILE REFERENCE: GX-0019-1 P
; CURRENT APPLICATION NUMBER: US/60/324,185
; CURRENT FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 35862
; SOFTWARE: PERL Program
; SEQ ID NO 4223
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: SNP00097881
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 1082325.7, 179, T->C
US-60-324-185-4223

Query Match
Best Local Similarity 1.5%; Score 40.4; DB 76; Length 51;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 240 TTCACCCAGAGAGAGGAGGTTGTGAGCCCTGTCAGAGGAGCCCTGCA 289
DB 2 TTCACCCAGAGAGAGGAGGTTGTGAGCCCTGTCAGAGGAGCCCTGCA 51

RESULT 16
```

```
US-60-213-359-20
; Sequence 20, Application US/60213359
; GENERAL INFORMATION:
; APPLICANT: Morris, Macdonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymor
; FILE REFERENCE: GX-0015 P
; CURRENT APPLICATION NUMBER: US/60/213,359
; CURRENT FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 7924
; SOFTWARE: PERL Program
; SEQ ID NO: 20
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: SNP00082481
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 010741.4, 633, A->G
US-60-213-359-20
```

```
Query Match 1.4%; Score 39.8; DB 65; Length 51;
Best Local Similarity 86.3%; Pred. No. 2.2;
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```
Oy 224 GGATGTGCTGTGTTACTTACCCAGAGAGTGAGGTTGTGAGCCCTGC 274
Db 1 GGATGTGCTGTGCTTCCACCCAGAGAGTGAGGTTGTGAGTTCTGC 51
```

```
RESULT 17
US-60-234-690-1769/c
; Sequence 1769, Application US/60234690
; GENERAL INFORMATION:
; APPLICANT: Morris, Macdonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; FILE REFERENCE: GX-0021 P
; CURRENT APPLICATION NUMBER: US/60/234,690
; CURRENT FILING DATE: 2000-09-21
; NUMBER OF SEQ ID NOS: 12060
; SOFTWARE: PERL Program
; SEQ ID NO: 1769
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: SNP00096187
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 1005180.1, 448, G->A
US-60-234-690-1769
```

```
Query Match 1.4%; Score 38.2; DB 67; Length 51;
Best Local Similarity 84.3%; Pred. No. 6.4;
Matches 43; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

```
Oy 2464 TGAGAACTGCTCTCCATTGGTGTGCTTCCCGATTGATCCCAACC 2514
Db 51 TGAGAACTGCTCTCTGTTGGCAAGCTTCTCTGATGTGATCCCAACC 1
```

```
RESULT 18
US-60-323-843-1769/c
```

```
; Sequence 1769, Application US/60323843
; GENERAL INFORMATION:
; APPLICANT: Morris, Macdonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; FILE REFERENCE: GX-0021-1 P
; CURRENT APPLICATION NUMBER: US/60/323,843
; CURRENT FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 12060
; SOFTWARE: PERL Program
; SEQ ID NO: 1769
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: SNP00096187
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 1005180.1, 448, G->A
US-60-323-843-1769
```

```
Query Match 1.4%; Score 38.2; DB 76; Length 51;
Best Local Similarity 84.3%; Pred. No. 6.4;
Matches 43; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

```
Oy 2464 TGAGAACTGCTCTCCATTGGTGTGCTTCCCGATTGATCCCAACC 2514
Db 51 TGAGAACTGCTCTCTGTTGGCAAGCTTCTCTGATGTGATCCCAACC 1
```

```
RESULT 19
US-60-324-185-26975
; Sequence 26975, Application US/60324185
; GENERAL INFORMATION:
; APPLICANT: Morris, Macdonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; FILE REFERENCE: GX-0019-1 P
; CURRENT APPLICATION NUMBER: US/60/324,185
; CURRENT FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 35862
; SOFTWARE: PERL Program
; SEQ ID NO: 26975
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: SNP00114633
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 399311.5, 1432, C->G
US-60-324-185-26975
```

```
Query Match 1.3%; Score 35.6; DB 76; Length 51;
Best Local Similarity 82.0%; Pred. No. 36;
Matches 41; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
```

```
Oy 1080 ACACACTCAGGGGAGAAACCTTATGTGTGCAAGATGTGACGAGGCTT 1129
Db 2 ACACACTCAGGGGAGAAACCTTGTGTGTAGAGATGTGCGCAAGATT 51
```

```
RESULT 20
US-60-213-359-2531
; Sequence 2531, Application US/60213359
```


GENERAL INFORMATION:
APPLICANT: MORRIS, Macdonald
APPLICANT: Lal, Preeti
TITLE OF INVENTION: Method for the identification of sequence polymorphisms using
TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymor
TITLE OF INVENTION: Identified thereby
FILE REFERENCE: GX-0015 P
CURRENT APPLICATION NUMBER: US/60/213,359
CURRENT FILING DATE: 2000-06-21
NUMBER OF SEQ ID NOS: 7924
SOFTWARE: PERL Program
SEQ ID NO 2531
LENGTH: 51
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: SNP0077379
NAME/KEY: snp
LOCATION: 26
OTHER INFORMATION: 481631.7, 204, C->T
US-60-213-359-2531

Query Match 1.3% Score 35; DB 65; Length 51;
Best Local Similarity 80.4% Pred. No. 54;
Matches 41; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Oy 278 GAGGACCCCTGACAGGAGTGTGCTGATATACCATGGTCTC 328
Db 1 GAGGACTCTATACAGGAGCTGATTTGGAGATTATAGAACCTGGTCTC 51

RESULT 21
US-09-908-975-6663
Sequence 6663, Application US/09908975
GENERAL INFORMATION:
APPLICANT: SHOSHAN, Avi
APPLICANT: WASSERMAN, Alon
APPLICANT: MINTZ, Eli
APPLICANT: MINTZ, Liat
APPLICANT: FAIGLER, Simchon
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
FILE REFERENCE: 36688-0005
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6663
LENGTH: 60
TYPE: DNA
ORGANISM: Homo sapiens
US-09-908-975-6663

Query Match 1.3% Score 35; DB 34; Length 60;
Best Local Similarity 74.6% Pred. No. 58;
Matches 44; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Oy 1041 GGCCTTACGTGAGTCAACCTGATCAGATCAGAGACACTGAGGAGAAACC 1099
Db 1 GCCTTTCCAGAGTGCACCTCAGATCAGAGATGCACACAGGGGAGAAACC 59

RESULT 22
US-09-908-975A-6663
Sequence 6663, Application US/09908975A
GENERAL INFORMATION:
APPLICANT: SHOSHAN, Avi

APPLICANT: WASSERMAN, Alon
APPLICANT: MINTZ, Eli
APPLICANT: MINTZ, Liat
APPLICANT: FAIGLER, Simchon
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLI
TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
FILE REFERENCE: 36688-0006
CURRENT APPLICATION NUMBER: US/09/908,975A
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6663
LENGTH: 60
TYPE: DNA
ORGANISM: Homo sapiens
US-09-908-975A-6663

Query Match 1.3% Score 35; DB 34; Length 60;
Best Local Similarity 74.6% Pred. No. 58;
Matches 44; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Oy 1041 GGCCTTACGTGAGTCAACCTGATCAGATCAGAGACACTGAGGAGAAACC 1099
Db 1 GCCTTTCCAGAGTGCACCTCAGATCAGAGATGCACACAGGGGAGAAACC 59

RESULT 23
US-60-287-724-6663
Sequence 6663, Application US/60287724
GENERAL INFORMATION:
APPLICANT: SHOSHAN, Avi
APPLICANT: WASSERMAN, Alon
APPLICANT: MINTZ, Eli
APPLICANT: MINTZ, Liat
APPLICANT: FAIGLER, Simchon
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLI
TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
FILE REFERENCE: 36688-0004
CURRENT APPLICATION NUMBER: US/60/287,724
CURRENT FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6663
LENGTH: 60
TYPE: DNA
ORGANISM: Homo sapiens
US-60-287-724-6663

Query Match 1.3% Score 35; DB 72; Length 60;
Best Local Similarity 74.6% Pred. No. 58;
Matches 44; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Oy 1041 GGCCTTACGTGAGTCAACCTGATCAGATCAGAGACACTGAGGAGAAACC 1099
Db 1 GCCTTTCCAGAGTGCACCTCAGATCAGAGATGCACACAGGGGAGAAACC 59

RESULT 24
US-09-726-173A-4584
Sequence 4584, Application US/09726173A
GENERAL INFORMATION:
APPLICANT: Shinkels, Richard A.
APPLICANT: Leach, Martin D.
TITLE OF INVENTION: NUCLEIC ACIDS CONTAINING SINGLE NUCLEOTIDE ACID POLYMORPHISMS AND
FILE REFERENCE: 15966-600
CURRENT APPLICATION NUMBER: US/09/726,173A
CURRENT FILING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: 60/168,138

```
; PRIOR FILING DATE: 1999-11-30
; NUMBER OF SEQ ID NOS: 7024
; SOFTWARE: Curagen Patent Formatter Version 0.9
; SEQ ID NO 4584
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (26)..(0)
; OTHER INFORMATION: 2 of 2 allelic variants (4583 is other entry)
; NAME/KEY: misc.feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Accession number cg43960167
US-09-726-173A-4584

Query Match
Best Local Similarity 1.2%; Score 34.6; DB 29; Length 51;
Matches 40; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db
1 AGACAATGCTAGGCGAGATAGGGGTGCTACCTGCTGAACCCACCT 2423

RESULT 25
US-60-324-185-4342
; Sequence 4342, Application US/60324185
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; FILE REFERENCE: GX-0019-1 P
; CURRENT FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 35862
; SOFTWARE: PERL Program
; SEQ ID NO 4342
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: SNP00121020
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 1085739.1, 1554, A->G
US-60-324-185-4342

Query Match
Best Local Similarity 1.2%; Score 33.6; DB 76; Length 51;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db
1056 TCAACCGCATCAGACATCAGAGACACACTAGGGGGAACCTTAT 1103
3 TCAACCTTATCAGACATCAGAGATCATAGTGGGGAGAACCTTAT 50

RESULT 26
US-60-172-360-29152
; Sequence 29152, Application US/60172360
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; FILE REFERENCE: GX-0007 P
; CURRENT APPLICATION NUMBER: US/60/172,360
```

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; CURRENT FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 29838
; SOFTWARE: PERL Program
; SEQ ID NO 29152
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: SNP00043257
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 430544.1, 203, T->G
US-60-172-360-29152

Query Match
Best Local Similarity 1.2%; Score 33.4; DB 61; Length 51;
Matches 37; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db
213 GTGGCATTCAGGAGATGTGCTGTACTTCACCCAGAGAGT 255
9 GTGGCTTGATGATGTGCTGTGACTTCACCCAGAGAGT 51

RESULT 27
US-60-250-830-1043
; Sequence 1043, Application US/60250830
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; FILE REFERENCE: GX-0020 P
; CURRENT FILING DATE: 2000-11-04
; NUMBER OF SEQ ID NOS: 3246
; SOFTWARE: PERL Program
; SEQ ID NO 1043
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: SNP00121038
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 1079415.2, 442, G->A
US-60-250-830-1043

Query Match
Best Local Similarity 1.2%; Score 33.4; DB 69; Length 51;
Matches 40; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Db
229 TGGCTGTACTTCACCCAGAGAGTGTGTTGACCCCTCTCAGA 279
1 TGGCTGTGACTTCACCCAGAGAGATGACTTCTGTGATCAACTCAGA 51

RESULT 28
US-60-323-966-1043
; Sequence 1043, Application US/60323966
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; FILE REFERENCE: GX-0020-1 P
; CURRENT APPLICATION NUMBER: US/60/323,966
```

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; CURRENT FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 3246
; SOFTWARE: PERL Program
; SEQ ID NO 1043
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: SNP0121038
; LOCATION: 26
; OTHER INFORMATION: 1079415.2, 442, G->A
; US-60-323-966-1043

Query Match
Best Local Similarity 1.2%; Score 33.4; DB 76; Length 51;
Matches 40; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 229 TGGCTGTGACTTACCCAGGAGAGTGGAGTGTGAGCCCTGCTCAGA 279
Db 1 TGGCTGTGACTTACCCAGGAGAGTGGAGTGTGCTGCTGATCAACTCAGA 51

RESULT 29
; US-09-726-173A-4583
; Sequence 4583, Application US/09726173A
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Leach, Martin D.
; TITLE OF INVENTION: NUCLEIC ACIDS CONTAINING SINGLE NUCLEIC ACID POLYMORPHISMS AND ME
; TITLE OF INVENTION: USE THEREOF
; FILE REFERENCE: 15966-600
; CURRENT APPLICATION NUMBER: US/09/726,173A
; CURRENT FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: 60/168,138
; NUMBER OF SEQ ID NOS: 7024
; SOFTWARE: Curagen Patent Formatter Version 0.9
; SEQ ID NO 4583
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (26)..(0)
; OTHER INFORMATION: 1 of 2 allelic variants (4584 is other entry)
; NAME/KEY: misc.feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Accession number C943960167
; US-09-726-173A-4583

Query Match
Best Local Similarity 1.2%; Score 33; DB 29; Length 51;
Matches 39; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 2375 AGTGAATGCCAGCAGATAGGGGTGCTACTGTGTAACCCCACT 2423
Db 1 AGACAATGCCCTAGCAGATAGGGGAGGTCAACAGTGAACCCCACT 49

RESULT 30
; US-60-172-373-5373
; Sequence 5373, Application US/60172373
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymor
; FILE REFERENCE: GX-0006 P
; CURRENT APPLICATION NUMBER: US/60/172,373
```

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; CURRENT FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 25,772
; SOFTWARE: PERL Program
; SEQ ID NO 5373
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: SNP00020062
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 414789.1, 931, T->C
; US-60-172-373-5373

Query Match
Best Local Similarity 1.2%; Score 32.6; DB 61; Length 51;
Matches 38; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1663 AGAGACACACTCAGGGGAGAGCCATTGTATGCTGAGTGTGCA 1709
Db 1 AGAGACACACTCAGGGGAGAGCCATTGATGATGAGTGTGCA 47

RESULT 31
; US-60-213-360-2773
; Sequence 2773, Application US/60213360
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Poly
; FILE REFERENCE: GX-0014 P
; CURRENT APPLICATION NUMBER: US/60/213,360
; CURRENT FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 8347
; SOFTWARE: PERL Program
; SEQ ID NO 2773
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: SNP00087205
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 1078555.7, 1819, C->G
; US-60-213-360-2773

Query Match
Best Local Similarity 1.2%; Score 32.6; DB 65; Length 51;
Matches 38; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1659 CACCAGACACACTCAGGGGAGAGCCATTGTATGCTGAGTGTG 1705
Db 5 CATCAGAGACACACACAGGGGAGAGCCCTTTGATGATGCCGATG 51

RESULT 32
; US-60-278-258-5877
; Sequence 5877, Application US/60278258
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide
; FILE REFERENCE: GX-0010-1 P
; CURRENT APPLICATION NUMBER: US/60/278,258
```

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; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 17730
; SOFTWARE: PERL Program
; SEQ ID NO 5877
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: SNP00065280
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 1090204.1, 730, A->G
US-60-278-258-5877

Query Match
Best Local Similarity 1.2%; Score 32.4; DB 71; Length 51;
Matches 39; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Oy 1071 CATCAGAGACACTCAGGGAGAAACCTTATGTGTGCAAGATTGTGG 1120
    ||||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Db 1 CATCAGAGATACACACTGTGTGAGACCCCTATGATGTAGAGATGTGG 50

RESULT 33
US-60-324-185-4224
; Sequence 4224, Application US/60324185
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preelt
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; FILE REFERENCE: GX-0019-1 P
; CURRENT APPLICATION NUMBER: US/60/324,185
; CURRENT FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 35862
; SOFTWARE: PERL Program
; SEQ ID NO 4224
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: SNP00097882
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 1082325.7, 1433, A->G
US-60-324-185-4224

Query Match
Best Local Similarity 1.2%; Score 32.4; DB 76; Length 51;
Matches 39; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Oy 1239 CACGAGAGGCGCACACTGTCGAGAGAGCTTATGTTTGGAGGATGTGG 1288
    || | || | || | || | || | || | || | || | || | || | || |
Db 2 CACAGCGGACACACACTGTGGAGAGCCGTTATGTTGTGGGTGTGG 51

RESULT 34
US-60-324-185-6741
; Sequence 6741, Application US/60324185
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preelt
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; FILE REFERENCE: GX-0019-1 P
; CURRENT APPLICATION NUMBER: US/60/324,185
; CURRENT FILING DATE: 2001-09-21
```

```

; NUMBER OF SEQ ID NOS: 35862
; SOFTWARE: PERL Program
; SEQ ID NO 6741
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: SNP00118792
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 1142546.1, 616, G->A
US-60-324-185-6741

Query Match
Best Local Similarity 1.2%; Score 32.4; DB 76; Length 51;
Matches 39; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Oy 1072 ATCAGAGACACACTCAGGGAGAAACCTTATGTGTGCAAGATTGTGA 1121
    || | || | || | || | || | || | || | || | || | || | || |
Db 1 ATATAGAACACATACAGGGAGAAACCCCTATGATGTATGATGATGTGA 50

RESULT 35
US-60-213-359-1622
; Sequence 1622, Application US/60213359
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preelt
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Poly
; FILE REFERENCE: GX-0015 P
; CURRENT APPLICATION NUMBER: US/60/213,359
; CURRENT FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 7924
; SOFTWARE: PERL Program
; SEQ ID NO 1622
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: SNP00089876
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 332474.3, 556, G->A
US-60-213-359-1622

Query Match
Best Local Similarity 1.2%; Score 32; DB 65; Length 51;
Matches 38; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Oy 276 CAGAGACCTTCACAGGAGGTGCTGTGAGACTTAAACCATCTG 323
    || || || || || || || || || || || || || || || || || || ||
Db 3 CAGAGACCCCTGTACCAGATGTATGCTGTGAGACTACAGCACCTG 50

RESULT 36
US-60-213-360-2926
; Sequence 2926, Application US/60213360
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preelt
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Poly
; FILE REFERENCE: GX-0014 P
; CURRENT APPLICATION NUMBER: US/60/213,360
; CURRENT FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 8347
```

```
SOFTWARE: PERL Program
SEQ ID NO 2926
LENGTH: 51
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: SNP00078765
LOCATION: 26
OTHER INFORMATION: 1085739.1, 1554, G->A
US-60-213-360-2926
```

```
Query Match
Best Local Similarity 79.2%; Score 32; DB 65; Length 51;
Matches 38; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
```

```
OY 1056 TCACACCTGATCAGACATCAGAGACACCTCAGGAGAAACCTTAT 1103
DB 3 TCACACCTGATCAGACATCAGAGAAATTCATAGTGGGAGAAACCTTAT 50
```

RESULT 37

```
US-60-230-830-822
Sequence 822, Application US/60250830
GENERAL INFORMATION:
APPLICANT: Morris, MacDonald
APPLICANT: Lal, Preeti
APPLICANT: Diep, Dinh
TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
FILE REFERENCE: GX-0020 P
CURRENT FILING DATE: 2000-11-04
NUMBER OF SEQ ID NOS: 3246
SOFTWARE: PERL Program
SEQ ID NO 822
LENGTH: 51
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: SNP00104016
LOCATION: 26
OTHER INFORMATION: 332474.3, 558, G->A
US-60-250-830-822
```

```
Query Match
Best Local Similarity 79.2%; Score 32; DB 69; Length 51;
Matches 38; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
```

```
OY 276 CAGAGACCTGACAGGAGGTGATGCTGAGACTTATACCATCTG 323
DB 3 CAGAGACCTGATCAGACGATGTAACTGTGAGAACTACACCATCTG 50
```

RESULT 38

```
US-60-323-966-822
Sequence 822, Application US/60323966
GENERAL INFORMATION:
APPLICANT: Morris, MacDonald
APPLICANT: Lal, Preeti
APPLICANT: Diep, Dinh
TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
FILE REFERENCE: GX-0020-1 P
CURRENT FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 3246
SOFTWARE: PERL Program
```

```
SEQ ID NO 822
LENGTH: 51
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: SNP00104016
LOCATION: 26
OTHER INFORMATION: 332474.3, 558, G->A
US-60-323-966-822
```

```
Query Match
Best Local Similarity 79.2%; Score 32; DB 76; Length 51;
Matches 38; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
```

```
OY 276 CAGAGACCTGACAGGAGGTGATGCTGAGACTTATACCATCTG 323
DB 3 CAGAGACCTGATCAGACGATGTAACTGTGAGAACTACACCATCTG 50
```

RESULT 39

```
US-60-172-373-5588
Sequence 5588, Application US/60172373
GENERAL INFORMATION:
APPLICANT: Morris, MacDonald
APPLICANT: Lal, Preeti
APPLICANT: Diep, Dinh
TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polym
FILE REFERENCE: GX-0006 P
CURRENT FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 25,772
SOFTWARE: PERL Program
SEQ ID NO 5588
LENGTH: 51
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: SNP00024052
LOCATION: 26
OTHER INFORMATION: 482033.2, 1229, C->A
US-60-172-373-5588
```

```
Query Match
Best Local Similarity 76.5%; Score 31.8; DB 61; Length 51;
Matches 39; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
```

```
OY 1200 TGTGGCAGACCTTACCTGCAAGTCAACCTCTTACCCACGAGAGCGG 1250
DB 1 TGTGGCCTGGGCTTACGACGACGAGTAAACCTCATCTCCACGAGAGCG 51
```

RESULT 40

```
US-60-213-360-2750/c
Sequence 2750, Application US/60213360
GENERAL INFORMATION:
APPLICANT: Morris, MacDonald
APPLICANT: Lal, Preeti
APPLICANT: Diep, Dinh
TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polym
FILE REFERENCE: GX-0014 P
CURRENT FILING DATE: 2000-06-21
NUMBER OF SEQ ID NOS: 8347
SOFTWARE: PERL Program
SEQ ID NO 2750
```

```

: LENGTH: 51
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: OTHER INFORMATION: Incyte ID No: SNP00088806
: NAME/KEY: snp
: LOCATION: 26
: OTHER INFORMATION: 1077932.1, 29, C->T
US-60-213-360-2750

Query Match
Best Local Similarity 1.1%; Score 31.8; DB 65; Length 51;
Best Local Similarity 76.5%; Pred. No. 4.5e+02;
Matches 39; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 1063 TGATCACACATCAGGACACATCAGGAGAAACCTATGTGTCAGG 1113
DB 51 TGATTGACATCAGCAGACTCACACAGGAGAAACCTATCAGTGAAG 1

RESULT 41
US-60-324-185-3926
: Sequence 3926, Application US/60324185
: GENERAL INFORMATION:
: APPLICANT: Morris, MacDonald
: APPLICANT: Lal, Preeti
: APPLICANT: Diep, Dinh
: TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
: TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
: FILE REFERENCE: GX-0019-1 P
: CURRENT APPLICATION NUMBER: US/60/324.185
: CURRENT FILING DATE: 2001-09-21
: NUMBER OF SEQ ID NOS: 35862
: SOFTWARE: PERL Program
: SEQ ID NO 3926
: LENGTH: 51
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: OTHER INFORMATION: Incyte ID No: SNP00112420
: NAME/KEY: snp
: LOCATION: 26
: OTHER INFORMATION: 1076673.1, 794, A->G
US-60-324-185-3926

Query Match
Best Local Similarity 1.1%; Score 31.6; DB 76; Length 51;
Best Local Similarity 89.5%; Pred. No. 5.2e+02;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1251 CACACTGGGAGAGCCTTATGTTGCAGGAGATGTGG 1288
DB 5 CACACTGGTGAAGCCTTACGTATGAGTGAATGTGG 42

RESULT 42
US-60-324-185-4044
: Sequence 4044, Application US/60324185
: GENERAL INFORMATION:
: APPLICANT: Morris, MacDonald
: APPLICANT: Lal, Preeti
: APPLICANT: Diep, Dinh
: TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
: TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
: FILE REFERENCE: GX-0019-1 P
: CURRENT APPLICATION NUMBER: US/60/324.185
: CURRENT FILING DATE: 2001-09-21
: NUMBER OF SEQ ID NOS: 35862
: SOFTWARE: PERL Program
: SEQ ID NO 4044
: LENGTH: 51
```

```

: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: OTHER INFORMATION: Incyte ID No: SNP00105120
: NAME/KEY: snp
: LOCATION: 26
: OTHER INFORMATION: 1079501.1, 272, G->A
US-60-324-185-4044

Query Match
Best Local Similarity 1.1%; Score 31.4; DB 76; Length 51;
Best Local Similarity 77.6%; Pred. No. 5.9e+02;
Matches 38; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 214 TGGATTGAGGATGTGGCTGTACTTACCCAGGAGAGTGGAGGT 262
DB 3 TGACCTTAAGAGATGTGGCTGTGATCTTCACTGAGAGAGAGTGGGCT 51

RESULT 43
US-09-908-975-6403
: Sequence 6403, Application US/09908975
: GENERAL INFORMATION:
: APPLICANT: SHOSHAN, AVI
: APPLICANT: WASSERMAN, ALON
: APPLICANT: MINTZ, ELLI
: APPLICANT: MINTZ, LIAT
: APPLICANT: FAIGLER, SIMCHON
: TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLI
: TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
: FILE REFERENCE: 36688-0005
: CURRENT APPLICATION NUMBER: US/09/908.975
: CURRENT FILING DATE: 2001-07-20
: PRIOR APPLICATION NUMBER: US 60/287,724
: PRIOR FILING DATE: 2001-05-02
: PRIOR APPLICATION NUMBER: US 60/221,607
: PRIOR FILING DATE: 2000-07-28
: NUMBER OF SEQ ID NOS: 32337
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 6403
: LENGTH: 60
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-908-975-6403

Query Match
Best Local Similarity 1.1%; Score 31; DB 34; Length 60;
Best Local Similarity 87.2%; Pred. No. 8.4e+02;
Matches 34; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1419 CACACAGGAGAGAACCTTATGTATGCACAGAGTGGG 1457
DB 15 CACACAGGAGAGAACCTTATGTATGCACAGAGTGGG 53

RESULT 44
US-09-908-975A-6403
: Sequence 6403, Application US/09908975A
: GENERAL INFORMATION:
: APPLICANT: SHOSHAN, AVI
: APPLICANT: WASSERMAN, ALON
: APPLICANT: MINTZ, ELLI
: APPLICANT: MINTZ, LIAT
: APPLICANT: FAIGLER, SIMCHON
: TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLI
: TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
: FILE REFERENCE: 36688-0006
: CURRENT APPLICATION NUMBER: US/09/908.975A
: CURRENT FILING DATE: 2001-07-20
: PRIOR APPLICATION NUMBER: US 60/287,724
: PRIOR FILING DATE: 2001-05-02
: PRIOR APPLICATION NUMBER: US 60/221,607
: PRIOR FILING DATE: 2000-07-28
: NUMBER OF SEQ ID NOS: 32337
```

SOFTWARE: PatentIn version 3.0
SEQ ID NO 6403
LENGTH: 60
TYPE: DNA
ORGANISM: Homo sapiens
US-09-908-975A-6403

Query Match
Best Local Similarity 1.1%; Score 31; DB 34; Length 60;
Pred. No. 8.4e+02;
Matches 34; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1419 CACACAGAGAGAGCCCTTATGATGACAGATGTGGC 1457
Db 15 CACACAGAGAGAGAGCCCTATGATGATGACAGAGTGTGGC 53

RESULT 45
US-60-287-724-6403
Sequence 6403, Application US/60287724
GENERAL INFORMATION:
APPLICANT: SHOSHAN, Avi
APPLICANT: WASSERMAN, Alon
APPLICANT: MINTZ, Eli
APPLICANT: FAIGLER, Simchon
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICING
FILE REFERENCE: 36688-0004
CURRENT APPLICATION NUMBER: US/60/287,724
CURRENT FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6403
LENGTH: 60
TYPE: DNA
ORGANISM: Homo sapiens
US-60-287-724-6403

Query Match
Best Local Similarity 1.1%; Score 31; DB 72; Length 60;
Pred. No. 8.4e+02;
Matches 34; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1419 CACACAGAGAGAGCCCTTATGATGACAGATGTGGC 1457
Db 15 CACACAGAGAGAGAGCCCTATGATGATGACAGAGTGTGGC 53

RESULT 46
US-60-324-185-731
Sequence 731, Application US/60324185
GENERAL INFORMATION:
APPLICANT: MORRIS, MacDonald
APPLICANT: Lai, Preeti
APPLICANT: Diep, Dinh
TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
FILE REFERENCE: GX-0019-1 P
CURRENT APPLICATION NUMBER: US/60/324,185
CURRENT FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 35862
SOFTWARE: PERL Program
SEQ ID NO 731
LENGTH: 51
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: SNP00120539
NAME/KEY: snp
LOCATION: 26
OTHER INFORMATION: 017463.1, 155, T->C
US-60-324-185-731

Query Match
Best Local Similarity 1.1%; Score 30.8; DB 76; Length 51;
Pred. No. 8.8e+02;
Matches 38; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 219 TTCAGGATGTGGCTGTGACTTCACCCAGAGAGAGTGTGTGAG 268
Db 1 TTAGAGAGATGTGGCTGTGAACTTCACCCAGAGAGAGTGTGTGAG 50

RESULT 47
US-09-953-198-448
Sequence 448, Application US/09953198
GENERAL INFORMATION:
APPLICANT: COMPUGEN LTD
TITLE OF INVENTION: DATA BASE OF SNP
FILE REFERENCE: 1351253
CURRENT APPLICATION NUMBER: US/09/953,198
CURRENT FILING DATE: 2001-08-12
NUMBER OF SEQ ID NOS: 979
SOFTWARE: PatentIn version 3.1
SEQ ID NO 448
LENGTH: 41
TYPE: DNA
ORGANISM: Homo sapiens
US-09-953-198-448

Query Match
Best Local Similarity 1.1%; Score 30.6; DB 36; Length 41;
Pred. No. 9e+02;
Matches 33; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 274 CTCAGAGAGACCTGCGACAGAGAGTGTGAGACTT 312
Db 1 CCCAGAGAGACCTGTGACAGAGAGTGTGAGACTT 39

RESULT 48
US-60-213-360-740
Sequence 740, Application US/60213360
GENERAL INFORMATION:
APPLICANT: MORRIS, MacDonald
APPLICANT: Lai, Preeti
APPLICANT: Diep, Dinh
TITLE OF INVENTION: Method for the identification of Sequence Polymorphisms Using
TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Poly
FILE REFERENCE: GX-0014 P
CURRENT APPLICATION NUMBER: US/60/213,360
CURRENT FILING DATE: 2000-06-21
NUMBER OF SEQ ID NOS: 8347
SOFTWARE: PERL Program
SEQ ID NO 740
LENGTH: 51
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: SNP00078224
NAME/KEY: snp
LOCATION: 26
OTHER INFORMATION: 1077201.1, 925, T->C
US-60-213-360-740

Query Match
Best Local Similarity 1.1%; Score 30.6; DB 65; Length 51;
Pred. No. 1e+03;
Matches 36; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1675 CAGGAGAGAGCCATTGTGATGTCAGTGTGAGAGGCTTTA 1719
Db 2 CTGGGAGAGAGCCCTTTGATGATGTCGAGAGTGTGAGAAATCTTCA 46

RESULT 49


```
US-60-250-830-971
: Sequence 971, Application US/60250830
: GENERAL INFORMATION:
: APPLICANT: Morris, MacDonald
: APPLICANT: Lal, Preeti
: APPLICANT: Diep, Dinh
: TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
: TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
: FILE REFERENCE: GX-0020 P
: CURRENT APPLICATION NUMBER: US/60/250,830
: CURRENT FILING DATE: 2000-11-04
: NUMBER OF SEQ ID NOS: 3246
: SOFTWARE: PERL Program
: SEQ ID NO 971
: LENGTH: 51
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID No: SNP00120410
: NAME/KEY: snp
: LOCATION: 26
: OTHER INFORMATION: 1080820.1, 293, T->G
US-60-250-830-971

Query Match      1.1%: Score 30.6; DB 69; Length 51;
Best Local Similarity 80.0%: Pred. No. 1e+03;
Matches 36; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY      235 TGTACTTCACCCAGAGAGAGTGTGTGAGCCCTGCTCAGA 279
Db      1 TGAAGTTCACCCAGAGAGAGTGTGTGAGCCCTGCTCAGA 45

RESULT 50
US-60-323-966-971
: Sequence 971, Application US/60323966
: GENERAL INFORMATION:
: APPLICANT: Morris, MacDonald
: APPLICANT: Lal, Preeti
: APPLICANT: Diep, Dinh
: TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING
: TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
: FILE REFERENCE: GX-0020-1 P
: CURRENT APPLICATION NUMBER: US/60/323,966
: CURRENT FILING DATE: 2001-09-21
: NUMBER OF SEQ ID NOS: 3246
: SOFTWARE: PERL Program
: SEQ ID NO 971
: LENGTH: 51
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID No: SNP00120410
: NAME/KEY: snp
: LOCATION: 26
: OTHER INFORMATION: 1080820.1, 293, T->G
US-60-323-966-971
```

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Query Match      1.1%: Score 30.6; DB 76; Length 51;
Best Local Similarity 80.0%: Pred. No. 1e+03;
Matches 36; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY      235 TGTACTTCACCCAGAGAGAGTGTGTGAGCCCTGCTCAGA 279
Db      1 TGAAGTTCACCCAGAGAGAGTGTGTGAGCCCTGCTCAGA 45
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Search completed: June 4, 2003, 12:07:57
Job time : 6069 secs

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OM nucleic - nucleic search, using sw model

Run on: June 4, 2003, 10:40:35 ; Search time 389 Seconds
(Without alignments)
9973.053 Million cell updates/sec

Title: US-09-898-556a-3
Perfect score: 2772
Sequence: 1 cagcgcgcttaagctgttg.....ttctaccatcctaccct 2772

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 870385 seqs, 699768693 residues

Total number of hits satisfying chosen parameters: 544182

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database :

Published Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	1.0	60	9	US-10-057-408-36 Sequence 36, Appl
2	26.6	1.0	56	9	US-10-057-408-49 Sequence 49, Appl
3	25.8	0.9	60	9	US-10-057-408-45 Sequence 45, Appl
4	25.6	0.9	56	9	US-10-057-408-40 Sequence 40, Appl
5	25	0.9	25	9	US-09-898-556a-6 Sequence 6, Appl
6	24.6	0.9	55	9	US-10-057-408-50 Sequence 50, Appl
7	24	0.9	58	9	US-09-775-049-14 Sequence 14, Appl
8	23.8	0.9	55	9	US-10-057-408-41 Sequence 41, Appl
9	23	0.8	60	9	US-09-906-393a-34 Sequence 34, Appl
10	22.4	0.8	54	9	US-10-055-713-24 Sequence 24, Appl
11	22.4	0.8	60	9	US-10-057-408-39 Sequence 39, Appl
12	22.4	0.8	60	9	US-10-057-408-48 Sequence 48, Appl
13	22.2	0.8	31	9	US-09-912-263-182 Sequence 182, Appl
14	21.4	0.8	60	9	US-09-906-393a-33 Sequence 33, Appl
15	21	0.8	21	9	US-09-898-556a-4 Sequence 4, Appl
16	21	0.8	31	10	US-09-801-274-1402 Sequence 1402, Ap
17	21	0.8	45	9	US-10-057-408-56 Sequence 56, Appl
18	21	0.8	59	9	US-10-066-960-236 Sequence 236, App
19	21	0.8	59	9	US-09-849-928-236 Sequence 236, App

20	20.6	0.7	52	9	US-10-066-960-244 Sequence 244, App
21	20.6	0.7	52	9	US-09-849-928-244 Sequence 244, App
22	20.2	0.7	50	9	US-09-950-442-40 Sequence 40, Appl
23	20	0.7	20	9	US-09-898-556a-12 Sequence 12, Appl
24	20	0.7	20	9	US-09-898-556a-13 Sequence 13, Appl
25	20	0.7	20	9	US-09-898-556a-14 Sequence 14, Appl
26	20	0.7	20	9	US-09-898-556a-15 Sequence 15, Appl
27	20	0.7	20	9	US-09-898-556a-16 Sequence 16, Appl
28	20	0.7	20	9	US-09-898-556a-17 Sequence 17, Appl
29	20	0.7	20	9	US-09-898-556a-18 Sequence 18, Appl
30	20	0.7	20	9	US-09-898-556a-19 Sequence 19, Appl
31	20	0.7	20	9	US-09-898-556a-20 Sequence 20, Appl
32	20	0.7	20	9	US-09-898-556a-21 Sequence 21, Appl
33	20	0.7	20	9	US-09-898-556a-22 Sequence 22, Appl
34	20	0.7	20	9	US-09-898-556a-23 Sequence 23, Appl
35	20	0.7	20	9	US-09-898-556a-24 Sequence 24, Appl
36	20	0.7	20	9	US-09-898-556a-25 Sequence 25, Appl
37	20	0.7	20	9	US-09-898-556a-26 Sequence 26, Appl
38	20	0.7	20	9	US-09-898-556a-27 Sequence 27, Appl
39	20	0.7	20	9	US-09-898-556a-28 Sequence 28, Appl
40	20	0.7	20	9	US-09-898-556a-29 Sequence 29, Appl
41	20	0.7	20	9	US-09-898-556a-30 Sequence 30, Appl
42	20	0.7	20	9	US-09-898-556a-31 Sequence 31, Appl
43	20	0.7	20	9	US-09-898-556a-32 Sequence 32, Appl
44	20	0.7	20	9	US-09-898-556a-33 Sequence 33, Appl
45	20	0.7	20	9	US-09-898-556a-34 Sequence 34, Appl
46	20	0.7	20	9	US-09-898-556a-35 Sequence 35, Appl
47	20	0.7	20	9	US-09-898-556a-36 Sequence 36, Appl
48	20	0.7	20	9	US-09-898-556a-37 Sequence 37, Appl
49	20	0.7	20	9	US-09-898-556a-38 Sequence 38, Appl
50	20	0.7	20	9	US-09-898-556a-39 Sequence 39, Appl
51	20	0.7	20	9	US-09-898-556a-40 Sequence 40, Appl
52	20	0.7	20	9	US-09-898-556a-41 Sequence 41, Appl
53	20	0.7	20	9	US-09-898-556a-42 Sequence 42, Appl
54	20	0.7	20	9	US-09-898-556a-43 Sequence 43, Appl
55	20	0.7	20	9	US-09-898-556a-44 Sequence 44, Appl
56	20	0.7	20	9	US-09-898-556a-45 Sequence 45, Appl
57	20	0.7	20	9	US-09-898-556a-46 Sequence 46, Appl
58	20	0.7	20	9	US-09-898-556a-47 Sequence 47, Appl
59	20	0.7	20	9	US-09-898-556a-48 Sequence 48, Appl
60	20	0.7	20	9	US-09-898-556a-49 Sequence 49, Appl
61	20	0.7	20	9	US-09-898-556a-50 Sequence 50, Appl
62	20	0.7	20	9	US-09-898-556a-51 Sequence 51, Appl
63	20	0.7	20	9	US-09-898-556a-52 Sequence 52, Appl
64	20	0.7	20	9	US-09-898-556a-53 Sequence 53, Appl
65	20	0.7	20	9	US-09-898-556a-54 Sequence 54, Appl
66	20	0.7	20	9	US-09-898-556a-55 Sequence 55, Appl
67	20	0.7	20	9	US-09-898-556a-56 Sequence 56, Appl
68	20	0.7	20	9	US-09-898-556a-57 Sequence 57, Appl
69	20	0.7	20	9	US-09-898-556a-58 Sequence 58, Appl
70	20	0.7	20	9	US-09-898-556a-59 Sequence 59, Appl
71	20	0.7	20	9	US-09-898-556a-60 Sequence 60, Appl
72	20	0.7	20	9	US-09-898-556a-61 Sequence 61, Appl
73	20	0.7	20	9	US-09-898-556a-62 Sequence 62, Appl
74	20	0.7	20	9	US-09-898-556a-63 Sequence 63, Appl
75	20	0.7	20	9	US-09-898-556a-64 Sequence 64, Appl
76	20	0.7	20	9	US-09-898-556a-65 Sequence 65, Appl
77	20	0.7	20	9	US-09-898-556a-66 Sequence 66, Appl
78	20	0.7	20	9	US-09-898-556a-67 Sequence 67, Appl
79	20	0.7	20	9	US-09-898-556a-68 Sequence 68, Appl
80	20	0.7	20	9	US-09-898-556a-69 Sequence 69, Appl
81	20	0.7	20	9	US-09-898-556a-70 Sequence 70, Appl
82	20	0.7	20	9	US-09-898-556a-71 Sequence 71, Appl
83	20	0.7	20	9	US-09-898-556a-72 Sequence 72, Appl
84	20	0.7	20	9	US-09-898-556a-73 Sequence 73, Appl
85	20	0.7	20	9	US-09-898-556a-74 Sequence 74, Appl
86	20	0.7	20	9	US-09-898-556a-75 Sequence 75, Appl
87	20	0.7	20	9	US-09-898-556a-76 Sequence 76, Appl
88	20	0.7	20	9	US-09-898-556a-77 Sequence 77, Appl
89	20	0.7	20	9	US-09-898-556a-78 Sequence 78, Appl
90	20	0.7	20	9	US-09-898-556a-79 Sequence 79, Appl
91	20	0.7	20	9	US-09-898-556a-80 Sequence 80, Appl
92	20	0.7	20	9	US-09-898-556a-81 Sequence 81, Appl

93	20	0.7	20	9	US-09-898-556a-89	Sequence 89, Appl
94	20	0.7	31	10	US-09-801-274-1404	Sequence 1404, Ap
95	20	0.7	50	9	US-09-941-947A-54	Sequence 54, Appl
96	20	0.7	55	10	US-09-866-514-6	Sequence 6, Appl1
97	19.8	0.7	28	10	US-09-851-129A-13	Sequence 13, Appl
98	19.8	0.7	48	9	US-09-877-478-5464	Sequence 5464, Ap
99	19.8	0.7	57	9	US-09-500-700-47	Sequence 47, Appl
100	19.8	0.7	68	7	US-08-781-986A-1661	Sequence 1661, Ap
101	19.6	0.7	40	9	US-09-864-785-3163	Sequence 3163, Ap
102	19.4	0.7	45	9	US-10-057-408-13	Sequence 54, Appl
103	19.4	0.7	48	9	US-09-848-754A-7934	Sequence 7934, Ap
104	19.4	0.7	49	9	US-09-156-323-6	Sequence 6, Appl1
105	19.4	0.7	50	9	US-09-943-007A-9	Sequence 9, Appl1
106	19.4	0.7	54	9	US-10-287-919-1217	Sequence 1217, Ap
107	19.2	0.7	25	10	US-09-866-108-14627	Sequence 14627, A
108	19.2	0.7	25	10	US-09-866-108-14627	Sequence 14628, A
109	19.2	0.7	48	9	US-09-877-478-5531	Sequence 5531, Ap
110	19.2	0.7	57	9	US-10-198-069-30	Sequence 30, Appl
111	19.2	0.7	59	9	US-09-991-262-53	Sequence 53, Appl
112	19	0.7	19	9	US-09-898-556A-5	Sequence 5, Appl1
113	19	0.7	30	10	US-09-785-633A-80	Sequence 80, Appl
114	19	0.7	31	10	US-09-801-274-1405	Sequence 1405, Ap
115	19	0.7	46	9	US-10-199-330-13	Sequence 13, Appl
116	19	0.7	46	9	US-10-199-334-13	Sequence 43, Appl
117	19	0.7	48	9	US-10-057-408-43	Sequence 57, Appl
118	19	0.7	50	9	US-09-905-291A-57	Sequence 57, Appl
119	19	0.7	50	9	US-09-902-853-57	Sequence 57, Appl
120	19	0.7	50	9	US-09-907-824-57	Sequence 57, Appl
121	19	0.7	50	9	US-09-907-841-57	Sequence 57, Appl
122	19	0.7	50	9	US-09-904-011-57	Sequence 57, Appl
123	19	0.7	50	9	US-09-906-742-57	Sequence 57, Appl
124	19	0.7	50	9	US-09-906-838-57	Sequence 57, Appl
125	19	0.7	50	9	US-09-907-613-57	Sequence 57, Appl
126	19	0.7	50	9	US-09-907-942-57	Sequence 57, Appl
127	19	0.7	50	9	US-09-904-820-57	Sequence 57, Appl
128	19	0.7	50	9	US-09-904-859-57	Sequence 57, Appl
129	19	0.7	50	9	US-09-909-204-57	Sequence 57, Appl
130	19	0.7	50	9	US-09-904-786-57	Sequence 57, Appl
131	19	0.7	50	9	US-09-906-646-57	Sequence 57, Appl
132	19	0.7	50	9	US-09-906-700-57	Sequence 57, Appl
133	19	0.7	50	9	US-09-902-903-57	Sequence 57, Appl
134	19	0.7	50	9	US-09-903-749A-57	Sequence 57, Appl
135	19	0.7	50	9	US-09-903-786-57	Sequence 57, Appl
136	19	0.7	50	9	US-09-902-736-57	Sequence 57, Appl
137	19	0.7	50	9	US-09-904-119-57	Sequence 57, Appl
138	19	0.7	50	9	US-09-904-956-57	Sequence 57, Appl
139	19	0.7	50	9	US-09-907-794-57	Sequence 57, Appl
140	19	0.7	50	9	US-09-902-692-57	Sequence 57, Appl
141	19	0.7	50	9	US-09-903-520-57	Sequence 57, Appl
142	19	0.7	50	9	US-09-903-943-57	Sequence 57, Appl
143	19	0.7	50	9	US-09-904-466-57	Sequence 57, Appl
144	19	0.7	50	9	US-09-905-056-57	Sequence 57, Appl
145	19	0.7	50	9	US-09-907-925-57	Sequence 57, Appl
146	19	0.7	50	9	US-09-904-553-57	Sequence 57, Appl
147	19	0.7	50	9	US-09-905-381-57	Sequence 57, Appl
148	19	0.7	50	9	US-09-909-064-57	Sequence 57, Appl
149	19	0.7	50	9	US-09-905-088-57	Sequence 57, Appl
150	19	0.7	50	9	US-09-907-575-57	Sequence 57, Appl
151	19	0.7	50	9	US-09-902-759-57	Sequence 57, Appl
152	19	0.7	50	9	US-09-905-075-57	Sequence 57, Appl
153	19	0.7	50	9	US-09-902-634-57	Sequence 57, Appl
154	19	0.7	50	9	US-09-902-713-57	Sequence 57, Appl
155	19	0.7	50	9	US-09-907-979-57	Sequence 57, Appl
156	19	0.7	50	9	US-09-907-615-57	Sequence 57, Appl
157	19	0.7	50	9	US-09-903-925-57	Sequence 57, Appl
158	19	0.7	50	9	US-09-906-760A-17	Sequence 14, Appl
159	19	0.7	50	10	US-09-828-366-14	Sequence 57, Appl
160	19	0.7	50	10	US-09-909-320-57	Sequence 57, Appl
161	19	0.7	55	9	US-09-909-088B-57	Sequence 188, App
162	19	0.7	55	9	US-09-747-377-188	Sequence 188, App
163	19	0.7	55	9	US-10-105-613-188	Sequence 32, Appl
164	19	0.7	60	9	US-09-906-933A-32	Sequence 47, Appl
165	18.8	0.7	40	9	US-10-057-558-47	Sequence 47, Appl
166	18.8	0.7	49	9	US-09-151-771-6	Sequence 6, Appl1
167	18.8	0.7	51	10	US-09-808-356-45	Sequence 45, Appl
168	18.6	0.7	25	10	US-09-866-108-14626	Sequence 14626, A
169	18.6	0.7	38	9	US-09-930-423-2600	Sequence 2600, Ap
170	18.6	0.7	42	9	US-10-223-074-70	Sequence 70, Appl
171	18.6	0.7	46	10	US-09-738-841-21	Sequence 21, Appl
172	18.6	0.7	50	9	US-09-754-066-15	Sequence 15, Appl
173	18.6	0.7	51	10	US-09-826-630-7	Sequence 8, Appl1
174	18.6	0.7	51	10	US-09-921-209-72	Sequence 72, Appl
175	18.6	0.7	55	9	US-09-826-630-8	Sequence 5140, Ap
176	18.6	0.7	56	7	US-08-781-986A-5140	Sequence 186, App
177	18.4	0.7	31	9	US-09-931-325-186	Sequence 2508, Ap
178	18.4	0.7	38	9	US-09-730-289A-2308	Sequence 5, Appl1
179	18.4	0.7	45	9	US-10-209-932-5	Sequence 6616, Ap
180	18.4	0.7	48	9	US-09-780-553A-6616	Sequence 9, Appl1
181	18.4	0.7	59	10	US-09-877-804-9	Sequence 1803, Ap
182	18.4	0.7	60	7	US-08-781-986A-1803	Sequence 2001, Ap
183	18.4	0.7	60	9	US-09-902-941-2001	Sequence 19, Appl
184	18.4	0.7	60	9	US-09-979-999-19	Sequence 2001, Ap
185	18.4	0.7	60	9	US-10-017-754-2001	Sequence 30, Appl
186	18.2	0.7	25	10	US-09-866-108-14629	Sequence 14629, A
187	18.2	0.7	34	10	US-09-730-857-30	Sequence 2, Appl1
188	18.2	0.7	43	10	US-09-994-420-2	Sequence 6, Appl1
189	18.2	0.7	43	12	US-10-082-032-2	Sequence 239, App
190	18.2	0.7	45	10	US-09-760-008A-6	Sequence 239, App
191	18.2	0.7	46	9	US-09-992-599-239	Sequence 239, App
192	18.2	0.7	46	9	US-09-989-299A-239	Sequence 239, App
193	18.2	0.7	46	9	US-09-989-733-239	Sequence 239, App
194	18.2	0.7	46	9	US-09-990-444-239	Sequence 239, App
195	18.2	0.7	46	9	US-09-989-733-239	Sequence 239, App
196	18.2	0.7	46	9	US-09-990-436-239	Sequence 239, App
197	18.2	0.7	46	9	US-09-991-181-239	Sequence 239, App
198	18.2	0.7	46	9	US-09-993-687-239	Sequence 239, App
199	18.2	0.7	46	9	US-09-989-734-239	Sequence 239, App
200	18.2	0.7	46	9	US-09-997-653-239	Sequence 239, App
201	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
202	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
203	18.2	0.7	46	9	US-09-990-438-239	Sequence 239, App
204	18.2	0.7	46	9	US-09-990-562-239	Sequence 239, App
205	18.2	0.7	46	9	US-09-997-428-239	Sequence 239, App
206	18.2	0.7	46	9	US-09-997-666-239	Sequence 239, App
207	18.2	0.7	46	9	US-09-990-711-239	Sequence 239, App
208	18.2	0.7	46	9	US-09-988-726-239	Sequence 239, App
209	18.2	0.7	46	9	US-09-990-437-239	Sequence 239, App
210	18.2	0.7	46	9	US-09-990-443-239	Sequence 239, App
211	18.2	0.7	46	9	US-09-997-746-239	Sequence 239, App
212	18.2	0.7	46	9	US-09-991-157-239	Sequence 239, App
213	18.2	0.7	46	9	US-09-991-172-239	Sequence 239, App
214	18.2	0.7	46	9	US-09-997-514-239	Sequence 239, App
215	18.2	0.7	46	9	US-09-990-443-239	Sequence 239, App
216	18.2	0.7	46	9	US-09-990-726-239	Sequence 239, App
217	18.2	0.7	46	9	US-09-997-559-239	Sequence 239, App
218	18.2	0.7	46	9	US-09-997-601-239	Sequence 239, App
219	18.2	0.7	46	9	US-09-989-729A-239	Sequence 239, App
220	18.2	0.7	46	9	US-09-990-440-239	Sequence 239, App
221	18.2	0.7	46	9	US-09-991-854-239	Sequence 239, App
222	18.2	0.7	46	9	US-09-997-349-239	Sequence 239, App
223	18.2	0.7	46	9	US-09-997-440-239	Sequence 239, App
224	18.2	0.7	46	9	US-09-997-628-239	Sequence 239, App
225	18.2	0.7	46	9	US-09-997-683-239	Sequence 239, App
226	18.2	0.7	46	9	US-09-993-469-239	Sequence 239, App
227	18.2	0.7	46	9	US-09-993-748-239	Sequence 239, App
228	18.2	0.7	46	9	US-09-997-942-239	Sequence 239, App
229	18.2	0.7	46	9	US-09-990-427-239	Sequence 239, App
230	18.2	0.7	46	9	US-09-990-439-239	Sequence 239, App
231	18.2	0.7	46	9	US-09-989-328-239	Sequence 239, App
232	18.2	0.7	46	9	US-09-993-983-239	Sequence 239, App
233	18.2	0.7	46	9	US-09-941-992-239	Sequence 239, App
234	18.2	0.7	46	9	US-09-992-921-239	Sequence 239, App
235	18.2	0.7	46	9	US-09-997-333-239	Sequence 239, App
236	18.2	0.7	46	10	US-09-997-384-239	Sequence 239, App
237	18.2	0.7	46	10	US-09-989-722-239	Sequence 239, App
238	18.2	0.7	46	10	US-09-989-723-239	Sequence 239, App
239	18.2	0.7	46	10	US-09-989-279-239	Sequence 239, App

C 239	18.2	0.7	46	10	US-09-989-727-239	Sequence 239, App	312	17.6	0.6	35	10	US-09-947-925a-9	Sequence 9, Appl1
C 240	18.2	0.7	46	10	US-09-989-731-239	Sequence 239, App	313	17.6	0.6	38	10	US-09-930-423-445	Sequence 2415, Ap
C 241	18.2	0.7	46	10	US-09-989-732-239	Sequence 239, App	C 314	17.6	0.6	38	10	US-09-842-552-42	Sequence 44, Appl
C 242	18.2	0.7	46	10	US-09-991-073-239	Sequence 239, App	C 315	17.6	0.6	39	10	US-09-264-468b-11	Sequence 11, Appl
C 243	18.2	0.7	46	10	US-09-990-442-239	Sequence 239, App	C 316	17.6	0.6	40	9	US-10-150-051-2	Sequence 2, Appl1
C 244	18.2	0.7	46	10	US-09-991-163-239	Sequence 239, App	C 317	17.6	0.6	42	9	US-10-168-050-9	Sequence 9, Appl1
C 245	18.2	0.7	46	10	US-09-993-604-239	Sequence 239, App	C 318	17.6	0.6	42	10	US-09-728-466-25	Sequence 25, Appl
C 246	18.2	0.7	46	10	US-09-990-456-239	Sequence 239, App	C 319	17.6	0.6	45	9	US-09-956-086-23	Sequence 23, Appl
C 247	18.2	0.7	46	10	US-09-989-721-239	Sequence 239, App	C 320	17.6	0.6	45	9	US-09-918-156-70	Sequence 23, Appl
C 248	18.2	0.7	48	9	US-10-066-960-194	Sequence 194, App	C 321	17.6	0.6	45	9	US-09-780-533a-5956	Sequence 70, Appl
C 249	18.2	0.7	48	9	US-10-138-838-68	Sequence 68, Appl	C 322	17.6	0.6	48	9	US-09-780-533a-5956	Sequence 5956, Ap
C 250	18.2	0.7	48	9	US-10-139-031-68	Sequence 68, Appl	C 323	17.6	0.6	48	9	US-09-877-478-5308	Sequence 5308, Ap
C 251	18.2	0.7	48	9	US-09-781-533A-5788	Sequence 5788, Ap	C 324	17.6	0.6	48	9	US-09-877-478-5791	Sequence 5791, Ap
C 252	18.2	0.7	48	9	US-09-849-928-194	Sequence 194, App	C 325	17.6	0.6	48	9	US-09-776-474-2677	Sequence 2677, Ap
C 253	18.2	0.7	48	9	US-09-849-478-5801	Sequence 5801, Ap	C 326	17.6	0.6	48	9	US-09-780-164-2522	Sequence 2522, Ap
C 254	18.2	0.7	48	9	US-09-877-478-5849	Sequence 5849, Ap	C 327	17.6	0.6	48	9	US-09-930-423-4516	Sequence 4516, Ap
C 255	18.2	0.7	48	9	US-10-138-905-68	Sequence 68, Appl	C 328	17.6	0.6	50	7	US-08-781-986A-2237	Sequence 2237, App
C 256	18.2	0.7	48	9	US-10-138-916-68	Sequence 68, Appl	C 329	17.6	0.6	50	10	US-09-742-693-9	Sequence 9, Appl1
C 257	18.2	0.7	48	9	US-09-976-800-68	Sequence 68, Appl	C 330	17.6	0.6	51	7	US-08-781-986A-2847	Sequence 2847, Ap
C 258	18.2	0.7	52	7	US-08-781-986A-1748	Sequence 1748, Ap	C 331	17.6	0.6	53	9	US-09-904-557-10	Sequence 10, Appl
C 259	18.2	0.7	53	9	US-10-085-056-37	Sequence 37, Appl	C 332	17.6	0.6	53	10	US-09-263-959-588	Sequence 588, App
C 260	18.2	0.7	54	9	US-10-055-713-25	Sequence 25, Appl	C 333	17.6	0.6	53	10	US-09-975-408-13	Sequence 13, Appl
C 261	18.2	0.7	58	7	US-08-781-986A-5156	Sequence 5156, Ap	C 334	17.6	0.6	53	12	US-10-075-579-13	Sequence 13, Appl
C 262	18.2	0.7	60	9	US-09-907-111-277	Sequence 277, App	C 335	17.6	0.6	55	7	US-08-781-986A-2677	Sequence 2677, Ap
C 263	18.2	0.7	60	9	US-09-741-744A-143	Sequence 143, App	C 336	17.6	0.6	57	10	US-09-927-121B-68	Sequence 68, Appl
C 264	18	0.6	26	9	US-09-915-043-42	Sequence 42, Appl	C 337	17.6	0.6	57	10	US-09-850-165-27	Sequence 27, Appl
C 265	18	0.6	26	9	US-09-828-062-30	Sequence 30, Appl	C 338	17.6	0.6	58	7	US-08-781-986A-2018	Sequence 2018, Ap
C 266	18	0.6	43	9	US-10-081-408-7	Sequence 7, Appl1	C 339	17.6	0.6	60	9	US-09-841-513-19	Sequence 19, Appl
C 267	18	0.6	45	9	US-10-057-408-42	Sequence 42, Appl	C 340	17.6	0.6	60	9	US-09-994-064-49	Sequence 49, Appl
C 268	18	0.6	46	9	US-10-076-631-4	Sequence 4, Appl1	C 341	17.6	0.6	60	9	US-10-057-408-46	Sequence 46, Appl
C 269	18	0.6	48	9	US-09-848-754A-8144	Sequence 8144, Ap	C 342	17.6	0.6	60	9	US-09-995-529-181	Sequence 181, App
C 270	18	0.6	48	9	US-09-848-754A-8449	Sequence 8449, Ap	C 343	17.4	0.6	31	10	US-09-801-274-1723	Sequence 1723, App
C 271	18	0.6	48	9	US-09-930-423-4188	Sequence 4188, Ap	C 344	17.4	0.6	36	9	US-10-056-414-516	Sequence 516, App
C 272	18	0.6	49	9	US-09-952-060-18	Sequence 18, Appl	C 345	17.4	0.6	36	10	US-09-375-924C-8	Sequence 8, Appl1
C 273	18	0.6	49	10	US-09-753-436-72	Sequence 72, Appl	C 346	17.4	0.6	37	9	US-10-287-919-738	Sequence 738, App
C 274	18	0.6	53	9	US-09-918-156-60	Sequence 60, Appl	C 347	17.4	0.6	38	9	US-09-877-478-3724	Sequence 3724, Ap
C 275	18	0.6	60	7	US-08-781-986A-3448	Sequence 3448, Ap	C 348	17.4	0.6	38	9	US-09-848-754A-5040	Sequence 5040, Ap
C 276	18	0.6	60	9	US-09-907-111-256	Sequence 256, App	C 349	17.4	0.6	38	9	US-09-776-474-1533	Sequence 1533, Ap
C 277	18	0.6	60	9	US-10-059-271-60	Sequence 60, App	C 350	17.4	0.6	39	9	US-10-129-709-5	Sequence 5, Appl1
C 278	18	0.6	60	9	US-09-888-413-26	Sequence 26, Appl	C 351	17.4	0.6	42	9	US-10-043-573-131	Sequence 131, App
C 279	17.8	0.6	31	9	US-09-912-263-503	Sequence 503, App	C 352	17.4	0.6	42	9	US-09-954-594A-8	Sequence 8, Appl1
C 280	17.8	0.6	31	10	US-09-801-274-1403	Sequence 1403, Ap	C 353	17.4	0.6	42	9	US-09-954-594A-8	Sequence 8, Appl1
C 281	17.8	0.6	38	9	US-09-930-423-2953	Sequence 2953, Ap	C 354	17.4	0.6	42	9	US-09-974-685-8	Sequence 8, Appl1
C 282	17.8	0.6	40	9	US-10-150-051-4	Sequence 4, Appl1	C 355	17.4	0.6	42	9	US-09-974-685-8	Sequence 8, Appl1
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C 286	17.8	0.6	47	9	US-10-269-229-9	Sequence 9, Appl1	C 359	17.4	0.6	47	9	US-09-966-782A-34	Sequence 34, Appl
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C 289	17.8	0.6	48	9	US-09-877-478-5639	Sequence 5639, Ap	C 362	17.4	0.6	48	9	US-09-780-164-2347	Sequence 2347, Ap
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C 292	17.8	0.6	49	9	US-10-152-297-16	Sequence 16, Appl	C 365	17.4	0.6	51	10	US-09-969-002-43	Sequence 43, Appl
C 293	17.8	0.6	49	9	US-10-152-297-17	Sequence 17, Appl	C 366	17.4	0.6	52	7	US-09-989-002-51	Sequence 51, Appl
C 294	17.8	0.6	49	10	US-09-790-417-117	Sequence 117, App	C 367	17.4	0.6	52	7	US-08-781-986A-1855	Sequence 1855, Ap
C 295	17.8	0.6	49	10	US-09-790-417-118	Sequence 118, App	C 368	17.4	0.6	54	7	US-08-781-986A-5041	Sequence 5041, Ap
C 296	17.8	0.6	50	9	US-10-073-300-14	Sequence 14, Appl	C 369	17.4	0.6	54	10	US-09-785-962A-84	Sequence 84, Appl
C 297	17.8	0.6	50	9	US-10-073-300-15	Sequence 15, Appl	C 370	17.4	0.6	54	10	US-08-878-574-13496	Sequence 13496, A
C 298	17.8	0.6	51	10	US-09-859-104-4	Sequence 4, Appl1	C 371	17.4	0.6	54	10	US-09-825-012-31	Sequence 31, Appl
C 299	17.8	0.6	52	9	US-10-054-427-11	Sequence 11, Appl	C 372	17.4	0.6	55	10	US-09-969-617-11	Sequence 11, Appl
C 300	17.8	0.6	53	9	US-10-287-919-1219	Sequence 1219, Ap	C 373	17.4	0.6	57	10	US-09-922-261-147	Sequence 147, App
C 301	17.8	0.6	53	9	US-09-907-111-267	Sequence 267, App	C 374	17.4	0.6	57	10	US-09-850-165-33	Sequence 33, Appl
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C 305	17.8	0.6	54	9	US-10-233-996-29	Sequence 29, Appl	C 378	17.2	0.6	25	10	US-09-769-864-39	Sequence 39, Appl
C 306	17.8	0.6	59	10	US-09-878-574-1776	Sequence 1776, Ap	C 379	17.2	0.6	25	10	US-09-866-108-14630	Sequence 14630, A
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C 309	17.8	0.6	60	10	US-09-850-716A-370	Sequence 370, App	C 382	17.2	0.6	38	9	US-09-776-474-2038	Sequence 2038, Ap
C 310	17.8	0.6	60	10	US-09-897-778-370	Sequence 370, App	C 383	17.2	0.6	39	10	US-09-263-959-166	Sequence 166, App
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C 400	17.2	0.6	51	7	US-08-781-986A-5132	Sequence 5132, Appl1	C 473	17	0.6	60	9	US-09-954-692-26	Sequence 26, Appl1
C 401	17.2	0.6	51	10	US-09-866-778A-38	Sequence 38, Appl1	C 474	17	0.6	60	9	US-09-995-529-183	Sequence 183, Appl1
C 402	17.2	0.6	52	9	US-10-060-036-2090	Sequence 2090, Appl1	C 475	17	0.6	60	10	US-09-559-671A-26	Sequence 26, Appl1
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C 404	17.2	0.6	56	7	US-08-781-986A-1915	Sequence 1915, Appl1	C 477	16.8	0.6	25	12	US-10-046-722-11	Sequence 11, Appl1
C 405	17.2	0.6	57	9	US-10-156-604-15	Sequence 15, Appl1	C 478	16.8	0.6	28	9	US-10-125-635A-357	Sequence 357, Appl1
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C 421	17.2	0.6	33	9	US-09-943-123-4	Sequence 4, Appl1	C 494	16.8	0.6	41	9	US-09-997-931-28	Sequence 28, Appl1
C 422	17.2	0.6	35	9	US-10-287-919-736	Sequence 736, Appl1	C 495	16.8	0.6	42	10	US-09-765-272-553	Sequence 27, Appl1
C 423	17.2	0.6	35	9	US-09-864-785-1195	Sequence 1195, Appl1	C 496	16.8	0.6	44	9	US-09-913-238-27	Sequence 28, Appl1
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C 445	17.2	0.6	48	9	US-09-848-754A-8505	Sequence 8505, Appl1							
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Query Match 1.0%; Score 27; DB 9; Length 60;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 36; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1593 GGGGAGAACCATTTGATGTACGAGTGTGGCGAGGCTTTACCCGGAATCAACCTG 1652
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Db 1 GGGGAGAACCCGTATTAATGTCCGGAATGTGTAAAGTTTACCCNNNAGCNNNNNTTG 60

RESULT 2
US-10-057-408-49

; Sequence 49, Application US/10057408
; Publication No. US20030082561A1
; GENERAL INFORMATION:

; APPLICANT: Sera, Takashi

; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof

; FILE REFERENCE: 109845.135
; CURRENT APPLICATION NUMBER: US/10/057,408
; CURRENT FILING DATE: 2002-01-23

; PRIOR APPLICATION NUMBER: US 60/220,060
; PRIOR FILING DATE: 2000-07-21

; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 49

; LENGTH: 56
; TYPE: DNA

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Partial zinc finger domain oligomer
US-10-057-408-49

Query Match 1.0%; Score 26.6; DB 9; Length 56;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches 35; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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Db 1 GGGGAGAACCTTACAGTGTCCGGAATGCGGAAAGACCTTTAGTCGTA 49

RESULT 3

US-10-057-408-45

; Sequence 45, Application US/10057408
; Publication No. US20030082561A1
; GENERAL INFORMATION:

; APPLICANT: Sera, Takashi

; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof

; FILE REFERENCE: 109845.135
; CURRENT APPLICATION NUMBER: US/10/057,408
; CURRENT FILING DATE: 2002-01-23

; PRIOR APPLICATION NUMBER: US 60/220,060
; PRIOR FILING DATE: 2000-07-21

; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 45

; LENGTH: 60
; TYPE: DNA

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Partial zinc finger domain oligomer
US-10-057-408-45

Query Match 0.9%; Score 25.8; DB 9; Length 60;
Best Local Similarity 73.3%; Pred. No. 3.3e+02;
Matches 33; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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Db 1 GGGGAGAACCCGTATTAATGTCCGGAATGTGTAAAGTTTACG 45

RESULT 4
US-10-057-408-40

; Sequence 40, Application US/10057408
; Publication No. US20030082561A1
; GENERAL INFORMATION:

; APPLICANT: Sera, Takashi

; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof

; FILE REFERENCE: 109845.135
; CURRENT APPLICATION NUMBER: US/10/057,408
; CURRENT FILING DATE: 2002-01-23

; PRIOR APPLICATION NUMBER: US 60/220,060
; PRIOR FILING DATE: 2000-07-21

; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 40

; LENGTH: 56
; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: Partial zinc finger domain oligomer
; NAME/KEY: misc.feature

; LOCATION: (48)..(58)
; OTHER INFORMATION: Nucleotides 48-50 and 54-58 are "n" wherein "n" = g, a, t, or

US-10-057-408-40
Query Match 0.9%; Score 25.6; DB 9; Length 56;
Best Local Similarity 72.1%; Pred. No. 3.7e+02;
Matches 31; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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Db 7 AAGCCTTACAGTGTCCGGAATGCGGAGAGAGCTTTAGTNNNA 49

RESULT 5

US-09-898-556A-6

; Sequence 6, Application US/09898556A
; Publication No. US20030087849A1
; GENERAL INFORMATION:

; APPLICANT: C. Frank Benneft

; TITLE OF INVENTION: ANTISENSE MODULATION OF HKR1 EXPRESSION

; FILE REFERENCE: RTS-0248
; CURRENT APPLICATION NUMBER: US/09/898,556A
; CURRENT FILING DATE: 2001-07-03

; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 6

; LENGTH: 25
; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: PCR Probe
US-09-898-556A-6

Query Match 0.9%; Score 25; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2309 CTGCCCTTCGTCACGCTGTGATGCTG 2333
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Db 1 CTGCCCTTCGTCACGCTGTGATGCTG 25

RESULT 6

US-10-057-408-50/C

; Sequence 50, Application US/10057408
; Publication No. US20030082561A1
; GENERAL INFORMATION:

; APPLICANT: Sera, Takashi

; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof

; FILE REFERENCE: 109845.135
; CURRENT APPLICATION NUMBER: US/10/057,408
; CURRENT FILING DATE: 2002-01-23

; PRIOR APPLICATION NUMBER: US 60/220,060
; PRIOR FILING DATE: 2000-07-21

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; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 50
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Partial zinc finger domain oligomer
US-10-057-408-50

Query Match
Best Local Similarity 0.9%; Score 24.6; DB 9; Length 55;
Pred. No. 7.9e+02;
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 1211 CTTTACCTGAGTCAACCTCATTTACCAACGAGGCGGACACCTGGGAGAG 1265
DB 55 CTTTACTGCTAGTATGATGACTTACCAACCCACGACGACGCGGAGAG 1

RESULT 7
US-09-775-049-14/c
; Sequence 14, Application US/09775049
; Publication No. US20030036641A1
; GENERAL INFORMATION:
; APPLICANT: Padgett, Hal S.
; APPLICANT: Fitzmaurice, Wayne P.
; APPLICANT: Lindbo, John A.
; TITLE OF INVENTION: Methods For Homology-Driven Reassembly
; TITLE OF INVENTION: of Nucleic Acid Sequences
; FILE REFERENCE: P-Lg 4412
; CURRENT APPLICATION NUMBER: US/09/775,049
; CURRENT FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 58
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-775-049-14

Query Match
Best Local Similarity 0.9%; Score 24; DB 9; Length 58;
Pred. No. 1.3e+03;
Matches 33; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 2219 ATTCTGTGTGATTATGATGAGACTGTACTGTAGTATGATCT 2266
DB 55 ATCTGTGAGTAACATGCTTAATAATATGTACTGATGGGACATTTATCT 8

RESULT 8
US-10-057-408-41/c
; Sequence 41, Application US/10057408
; Publication No. US20030082561A1
; GENERAL INFORMATION:
; APPLICANT: Sera, Takashi
; TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
; FILE REFERENCE: 109845.135
; CURRENT APPLICATION NUMBER: US/10/057,408
; CURRENT FILING DATE: 2002-01-23
; PRIOR APPLICATION NUMBER: US 60/220,060
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 41
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Partial zinc finger domain oligomer
; NAME/KEY: misc.feature
LOCATION: (28)..(48)
```

```

; OTHER INFORMATION: Nucleotides 28-30, 37-42 and 46-48 are "n" wherein "n" -
; OTHER INFORMATION: g, a, t, or c
US-10-057-408-41

Query Match
Best Local Similarity 0.9%; Score 23.8; DB 9; Length 55;
Pred. No. 1.5e+03;
Matches 31; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

OY 1547 CTTTACCTGAGTCAACCTCATTTACCAACGAGGCGGACACGCGGAGAG 1601
DB 55 CTTTACTNNAGTNNNNNNNTTACANNNCACGACGACGCGGAGAG 1

RESULT 9
US-09-906-393A-34
; Sequence 34, Application US/09906393A
; Publication No. US20030039970A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; APPLICANT: Xiao, Wuhan
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906,393A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,761
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 34
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-906-393A-34

Query Match
Best Local Similarity 0.8%; Score 23; DB 9; Length 60;
Pred. No. 2.9e+03;
Matches 32; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 89 TCAGATCGCGCGCGCTTCATCTCTCTCTCTGAGACTT 135
DB 6 TCTGATCGGAGGTGATGACTGCTTACACACGCTTCGAGCTT 52

RESULT 10
US-10-055-713-24
; Sequence 24, Application US/10055713
; Publication No. US20030044957A1
; GENERAL INFORMATION:
; APPLICANT: JAMIESON, Andrew
; APPLICANT: Li, Guofu
; TITLE OF INVENTION: ZINC FINGER PROTEINS FOR DNA BINDING AND GENE
; TITLE OF INVENTION: REGULATION IN PLANTS
; FILE REFERENCE: 8325-0026 / 526-US1
; CURRENT APPLICATION NUMBER: US/10/055,713
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 60/263,445
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 60/290,716
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 24
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: oligonucleotide PB2
US-10-055-713-24

Query Match
Best Local Similarity 0.8%; Score 22.4; DB 9; Length 54;
Pred. No. 4.2e+03;
```


NUMBER OF SEQ ID NOS: 89
SEQ ID NO 4
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR Primer
US-09-898-556a-4

Query Match 0.8%; Score 21; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2276 TGAGAGAGATTGCTGCTCA 2296
1 TGAGAGAGATTGCTGCTCA 21

RESULT 16
US-09-801-274-1402
Sequence 1402, Application US/09801274
Patent No. US20020032319A1
GENERAL INFORMATION:
APPLICANT: Cargill, Michele
APPLICANT: Ireland, James S.
APPLICANT: Lander, Eric S.
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REFERENCE: 2825.2009-001
CURRENT APPLICATION NUMBER: US/09/801,274
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 60/187,510
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 60/206,129
PRIOR FILING DATE: 2000-05-22
NUMBER OF SEQ ID NOS: 1802
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1402
LENGTH: 31
TYPE: DNA
ORGANISM: Homo sapiens
US-09-801-274-1402

Query Match 0.8%; Score 21; DB 10; Length 31;
Best Local Similarity 77.4%; Pred. No. 8.6e+03;
Matches 24; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Db 1358 TTGCAGGAGTGTGAGCAAGCTTACCCAG 1388
1 TTGCAGGAGTGTGAGCAAGCTTACCCAG 31

RESULT 17
US-10-057-408-56/c
Sequence 56, Application US/10057408
Publication No. US20030082561A1
GENERAL INFORMATION:
APPLICANT: Sera, Takashi
TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof
FILE REFERENCE: 109845.135
CURRENT APPLICATION NUMBER: US/10/057,408
CURRENT FILING DATE: 2002-01-23
PRIOR APPLICATION NUMBER: US 60/220,060
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 69
SOFTWARE: Patentin version 3.0
SEQ ID NO 56
LENGTH: 45
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR primer
US-10-057-408-56

Query Match 0.8%; Score 21; DB 9; Length 45;
Best Local Similarity 82.8%; Pred. No. 1.1e+04;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 1239 CACCAAGCGCCGACACTGGGAGAGACC 1267
45 CACCAAGCGCCGACACTGGGAGAGACC 17

RESULT 18
US-10-066-960-236
Sequence 236, Application US/10066960
Publication No. US20030049644A1
GENERAL INFORMATION:
APPLICANT: PARMA, et al.
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
NUMBER OF SEQUENCES: 390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/066,960
FILING DATE: 04-Feb-2002
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/952,793
FILING DATE: 1999-DEC-03
APPLICATION NUMBER: PCT/US96/09455
FILING DATE: 05-JUNE-1995
APPLICATION NUMBER: 08/479,724
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/472,256
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/472,255
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/477,829
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX40C/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 236:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All C's are 2'-F cytosine
FEATURE:
OTHER INFORMATION: All U's are 2'-F uracil
SEQUENCE DESCRIPTION: SEQ ID NO: 236:
US-10-066-960-236

Query Match 0.8%; Score 21; DB 9; Length 59;
Best Local Similarity 62.2%; Pred. No. 1.3e+04;
Matches 28; Conservative 2; Mismatches 15; Indels 0; Gaps 0;

Db 140 CTTCTCCAGAGAGACACACGAGACCGAGAAATGCTACAG 184

Db 1 CUCACGAGCAAAAGUACUCACGGGACCAGGAGAUACAGACACAG 45

RESULT 19

US-09-849-928-236
; Sequence 236, Application US/09849928
; Publication No. US20030059769A1

GENERAL INFORMATION:

APPLICANT: PARMA, et al.

TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
TO LECTINS

NUMBER OF SEQUENCES: 390

CORRESPONDENCE ADDRESS:

ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA

ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB

COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS

SOFTWARE: Wordperfect 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/849,928

FILING DATE: 04-May-2001

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/952,793

FILING DATE: <unknown>

APPLICATION NUMBER: 08/479,724

FILING DATE: 07-JUNE-1995

APPLICATION NUMBER: 08/472,256

FILING DATE: 07-JUNE-1995

APPLICATION NUMBER: 08/472,255

FILING DATE: 07-JUNE-1995

APPLICATION NUMBER: 08/477,829

FILING DATE: 07-JUNE-1995

ATTORNEY/AGENT INFORMATION:

NAME: Barry J. Swanson

REGISTRATION NUMBER: 33,215

REFERENCE/DOCKET NUMBER: NEX40C/PCT

TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333

TELEFAX: (303) 793-3433

INFORMATION FOR SEQ ID NO: 236:

SEQUENCE CHARACTERISTICS:

LENGTH: 59 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: RNA

FEATURE:

OTHER INFORMATION: ALL C's are 2'-F cytosine

FEATURE:

OTHER INFORMATION: ALL U's are 2'-F uracil

SEQUENCE DESCRIPTION: SEQ ID NO: 236:

US-09-849-928-236

Query Match 0.8%; Score 21; DB 9; Length 59;

Best Local Similarity 62.2%; Pred. No. 1.3e+04;

Matches 28; Conservative 2; Mismatches 15; Indels 0; Gaps 0;

Db 140 CTCTCCAGAGAGCAGCAGGAGCAAAATGCTACAG 184

1 CUCACGAGCAAAAGUACUCACGGGACCAGGAGAUACAGACACAG 45

RESULT 20

US-10-066-960-244

; Sequence 244, Application US/10066960

Publication No. US20030049644A1

GENERAL INFORMATION:

APPLICANT: PARMA, et al.

TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
TO LECTINS

NUMBER OF SEQUENCES: 390

CORRESPONDENCE ADDRESS:

ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA

ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB

COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS

SOFTWARE: Wordperfect 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/066,960

FILING DATE: 04-Feb-2002

CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/952,793

FILING DATE: 1999-DEC-03

APPLICATION NUMBER: PCT/US96/09455

FILING DATE: 05-JUNE-1995

APPLICATION NUMBER: 08/479,724

FILING DATE: 07-JUNE-1995

APPLICATION NUMBER: 08/472,256

FILING DATE: 07-JUNE-1995

APPLICATION NUMBER: 08/472,255

FILING DATE: 07-JUNE-1995

APPLICATION NUMBER: 08/477,829

FILING DATE: 07-JUNE-1995

ATTORNEY/AGENT INFORMATION:

NAME: Barry J. Swanson

REGISTRATION NUMBER: 33,215

REFERENCE/DOCKET NUMBER: NEX40C/PCT

TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333

TELEFAX: (303) 793-3433

INFORMATION FOR SEQ ID NO: 244:

SEQUENCE CHARACTERISTICS:

LENGTH: 52 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: RNA

FEATURE:

OTHER INFORMATION: ALL C's are 2'-F cytosine

FEATURE:

OTHER INFORMATION: ALL U's are 2'-F uracil

SEQUENCE DESCRIPTION: SEQ ID NO: 244:

US-10-066-960-244

Query Match 0.7%; Score 20.6; DB 9; Length 52;

Best Local Similarity 65.7%; Pred. No. 1.7e+04;

Matches 23; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Db 580 CAGAGATCAGAAACACAGCAGATTCATTCGC 614

4 CAGCGGUCACAGAACACAUAGCUGACUACUACCGC 38

RESULT 21

US-09-849-928-244

; Sequence 244, Application US/09849928

; Publication No. US20030059769A1

GENERAL INFORMATION:

APPLICANT: PARMA, et al.

TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
TO LECTINS

NUMBER OF SEQUENCES: 390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 6.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/849,928
FILING DATE: 04-May-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/952,793
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/479,724
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/472,256
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/472,255
FILING DATE: 07-JUNE-1995
APPLICATION NUMBER: 08/477,829
FILING DATE: 07-JUNE-1995

ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX40C/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433

INFORMATION FOR SEQ ID NO: 244:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA

FEATURE:
OTHER INFORMATION: All C's are 2'-F cytosine

FEATURE:
OTHER INFORMATION: All U's are 2'-F uracil

SEQUENCE DESCRIPTION: SEQ ID NO: 244:
US-09-849-928-244

Query Match 0.7%; Score 20.6; DB 9; Length 52;
Best Local Similarity 65.7%; Pred.No. 1.7e+04;
Matches 23; Conservative 3; Mismatches 9; Indels 0; Gaps 0.

QY 580 CAGAAAGATCAGAAACACAGCAGATTCATCTGCG 614
|| | : ||||| ||||| ||||| : || : ||
Db 4 CAGCGGCGCAGAAACAUAUAGCGUAGUACUACGCG 38

RESULT 22
US-09-950-442-40/C
Sequence 40, Application US/09950442
Publication No. US20030027127A1
GENERAL INFORMATION:
APPLICANT: Farr, Spencer B.
Todd, Marque D.
TITLE OF INVENTION: METHODS AND DIAGNOSTIC KITS FOR
DETERMINING TOXICITY
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr. C/O FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York

```

1      COUNTRY: U.S.A.
2      ZIP: 10020
3
4      COMPUTER READABLE FORM:
5
6      MEDIUM TYPE: Floppy disk
7      COMPUTER: IBM PC compatible
8      OPERATING SYSTEM: PC-DOS/MS-DOS
9      SOFTWARE: PatentIn Release #1.0, Version #1.25
10
11     CURRENT APPLICATION DATA:
12
13     APPLICATION NUMBER: US/09/950,442
14     FILING DATE: 10-Sep-2001
15
16     CLASSIFICATION: <unknown>
17
18     PRIOR APPLICATION DATA:
19
20     APPLICATION NUMBER: 08/374,641
21     FILING DATE: 12-JUL-1995
22
23     ATTORNEY/AGENT INFORMATION:
24
25     NAME: Haley Jr., James F.
26     REGISTRATION NUMBER: 27,794
27     REFERENCE/DOCKET NUMBER: X-1 CIP
28
29     TELECOMMUNICATION INFORMATION:
30
31     TELEPHONE: (212) 596-9000
32     TELEFAX: (212) 596-9090
33
34     INFORMATION FOR SEQ ID NO: 40:
35
36     SEQUENCE CHARACTERISTICS:
37
38     LENGTH: 50 base pairs
39     TYPE: nucleic acid
40     STRANDEDNESS: single
41     TOPOLOGY: linear
42
43     MOLECULE TYPE: cDNA
44
45     HYPOTHETICAL: NO
46
47     SEQUENCE DESCRIPTION: SEQ ID NO: 40:
48     US-09-950-442-40

```

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Query Match      0.7%: Score 20.2; DB 9; Length 50;
Best Local Similarity 68.3%; Pred. No. 2.2e+04;
Matches 28; Conservative 0; Mismatches 13; Indels 0

Qy      2212 TGGAGACATCTCGTGTGATTAATCATGACACTGTACGG 2252
      ||||||| ||| ||| | | | ||| ||| |||
Db      48 TGCAGACATCTACTGAGTGTACCCGCTTGAAGACAGACTGG 8

RESULT 23
US-09-898-556A-12/c
; Sequence 12, Application US/09898556A
; Publication No. US20030087849A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKR1 EXPRESSION
; FILE REFERENCE: RTS-0248
; CURRENT APPLICATION NUMBER: US/09/898,556A
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-12

Query Match      0.7%: Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      33 GCCTCCCTCTTAAGGCTCTT 52
      ||||||| ||| ||| ||| ||| |||
Db      20 GCCTCCCTCTTAAGGCTCTT 1

RESULT 24
US-09-898-556A-13/c
; Sequence 13, Application US/09898556A

```

```
Publication No. US20030087849A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF HKRI EXPRESSION
FILE REFERENCE: RTS-0248
CURRENT APPLICATION NUMBER: US/09/898,556A
CURRENT FILING DATE: 2001-07-03
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 13
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-13

Query Match
Best Local Similarity 0.7%; Score 20; DB 9; Length 20;
Pred. No. 1.4e+04;
Matches 20; Conservative 0; Mismatches 0; Gaps 0; Indels 0;

QY 63 TGCTCCTGTACTGACTT 82
Db 20 TGCTCCTGTACTGACTT 1

RESULT 25
US-09-898-556A-14/C
Sequence 14, Application US/09898556A
Publication No. US20030087849A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF HKRI EXPRESSION
FILE REFERENCE: RTS-0248
CURRENT APPLICATION NUMBER: US/09/898,556A
CURRENT FILING DATE: 2001-07-03
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 14
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-14

Query Match
Best Local Similarity 0.7%; Score 20; DB 9; Length 20;
Pred. No. 1.4e+04;
Matches 20; Conservative 0; Mismatches 0; Gaps 0; Indels 0;

QY 70 TGTACCTGACTTCGCGCTT 89
Db 20 TGTACCTGACTTCGCGCTT 1

RESULT 26
US-09-898-556A-15/C
Sequence 15, Application US/09898556A
Publication No. US20030087849A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF HKRI EXPRESSION
FILE REFERENCE: RTS-0248
CURRENT APPLICATION NUMBER: US/09/898,556A
CURRENT FILING DATE: 2001-07-03
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 15
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
```

```
US-09-898-556A-15

Query Match
Best Local Similarity 0.7%; Score 20; DB 9; Length 20;
Pred. No. 1.4e+04;
Matches 20; Conservative 0; Mismatches 0; Gaps 0; Indels 0;

QY 131 GACCTTGGCCCTTCACAGGA 150
Db 20 GACCTTGGCCCTTCACAGGA 1

RESULT 27
US-09-898-556A-16/C
Sequence 16, Application US/09898556A
Publication No. US20030087849A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF HKRI EXPRESSION
FILE REFERENCE: RTS-0248
CURRENT APPLICATION NUMBER: US/09/898,556A
CURRENT FILING DATE: 2001-07-03
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 16
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-16

Query Match
Best Local Similarity 0.7%; Score 20; DB 9; Length 20;
Pred. No. 1.4e+04;
Matches 20; Conservative 0; Mismatches 0; Gaps 0; Indels 0;

QY 144 TCACAGAGAGACACTCAGGA 163
Db 20 TCACAGAGAGACACTCAGGA 1

RESULT 28
US-09-898-556A-17/C
Sequence 17, Application US/09898556A
Publication No. US20030087849A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF HKRI EXPRESSION
FILE REFERENCE: RTS-0248
CURRENT APPLICATION NUMBER: US/09/898,556A
CURRENT FILING DATE: 2001-07-03
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 17
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-17

Query Match
Best Local Similarity 0.7%; Score 20; DB 9; Length 20;
Pred. No. 1.4e+04;
Matches 20; Conservative 0; Mismatches 0; Gaps 0; Indels 0;

QY 308 GACCTATACCATCTGCTCT 327
Db 20 GACCTATACCATCTGCTCT 1

RESULT 29
US-09-898-556A-18/C
Sequence 18, Application US/09898556A
Publication No. US20030087849A1
```

```

; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKR1 EXPRESSION
; FILE REFERENCE: RTS-0248
; CURRENT APPLICATION NUMBER: US/09/898,556A
; NUMBER OF SEQ ID NOS: 89
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-18

Query Match
Best Local Similarity 0.7%; Score 20; DB 9; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 397 AGGAGAGAAATGTCCTG 416
Db 20 AGGAGAGAAATGTCCTG 1

RESULT 30
US-09-898-556A-19/c
; Sequence 19, Application US/09898556A
; Publication No. US20030087849A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKR1 EXPRESSION
; FILE REFERENCE: RTS-0248
; CURRENT APPLICATION NUMBER: US/09/898,556A
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-19

Query Match
Best Local Similarity 0.7%; Score 20; DB 9; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 411 CCACTGACCTCTGTCCAGA 430
Db 20 CCACTGACCTCTGTCCAGA 1

RESULT 31
US-09-898-556A-20/c
; Sequence 20, Application US/09898556A
; Publication No. US20030087849A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKR1 EXPRESSION
; FILE REFERENCE: RTS-0248
; CURRENT APPLICATION NUMBER: US/09/898,556A
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 20
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-20
```

```

Query Match
Best Local Similarity 0.7%; Score 20; DB 9; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 439 CAGAAATTCAGTACTGCTCC 458
Db 20 CAGAAATTCAGTACTGCTCC 1

RESULT 32
US-09-898-556A-21/c
; Sequence 21, Application US/09898556A
; Publication No. US20030087849A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKR1 EXPRESSION
; FILE REFERENCE: RTS-0248
; CURRENT APPLICATION NUMBER: US/09/898,556A
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-21

Query Match
Best Local Similarity 0.7%; Score 20; DB 9; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 470 GATTTCTCCAGTCAGCAAG 489
Db 20 GATTTCTCCAGTCAGCAAG 1

RESULT 33
US-09-898-556A-22/c
; Sequence 22, Application US/09898556A
; Publication No. US20030087849A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKR1 EXPRESSION
; FILE REFERENCE: RTS-0248
; CURRENT APPLICATION NUMBER: US/09/898,556A
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-22

Query Match
Best Local Similarity 0.7%; Score 20; DB 9; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 482 TCAGCAGACTCTCAGCCAC 501
Db 20 TCAGCAGACTCTCAGCCAC 1

RESULT 34
US-09-898-556A-23/c
; Sequence 23, Application US/09898556A
; Publication No. US20030087849A1
; GENERAL INFORMATION:
```

```

; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKR1 EXPRESSION
; FILE REFERENCE: RTS-0248
; CURRENT APPLICATION NUMBER: US/09/898,556a
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 23
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556a-23
```

```
Query Match
Best Local Similarity 100.0%; Score 20; DB 9; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 491 TCTCAGCCACATGTGTGC 510
DB 20 TCTCAGCCACATGTGTGC 1
```

```

RESULT 35
US-09-898-556a-24/c
; Sequence 24, Application US/09898556a
; Publication No. US20030087849A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKR1 EXPRESSION
; FILE REFERENCE: RTS-0248
; CURRENT APPLICATION NUMBER: US/09/898,556a
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 24
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556a-24
```

```
Query Match
Best Local Similarity 100.0%; Score 20; DB 9; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 506 GTGGCTGAGTCATCTCTCTC 525
DB 20 GTGGCTGAGTCATCTCTCTC 1
```

```

RESULT 36
US-09-898-556a-25/c
; Sequence 25, Application US/09898556a
; Publication No. US20030087849A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKR1 EXPRESSION
; FILE REFERENCE: RTS-0248
; CURRENT APPLICATION NUMBER: US/09/898,556a
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 25
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556a-25
```

```
Query Match
Best Local Similarity 100.0%; Score 20; DB 9; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 535 CAAGTTATGGCGAGGAAT 554
DB 20 CAAGTTATGGCGAGGAAT 1
```

```

RESULT 37
US-09-898-556a-26/c
; Sequence 26, Application US/09898556a
; Publication No. US20030087849A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKR1 EXPRESSION
; FILE REFERENCE: RTS-0248
; CURRENT APPLICATION NUMBER: US/09/898,556a
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 26
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556a-26
```

```
Query Match
Best Local Similarity 100.0%; Score 20; DB 9; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 594 CAACAGCAGATCCATCTCTG 613
DB 20 CAACAGCAGATCCATCTCTG 1
```

```

RESULT 38
US-09-898-556a-27/c
; Sequence 27, Application US/09898556a
; Publication No. US20030087849A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKR1 EXPRESSION
; FILE REFERENCE: RTS-0248
; CURRENT APPLICATION NUMBER: US/09/898,556a
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556a-27
```

```
Query Match
Best Local Similarity 100.0%; Score 20; DB 9; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 618 AGTGCAAGCAGATGAT 637
DB 20 AGTGCAAGCAGATGAT 1
```

```

RESULT 39
US-09-898-556a-28/c
; Sequence 28, Application US/09898556a
; Publication No. US20030087849A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
```

```

; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKR1 EXPRESSION
; FILE REFERENCE: RTS-0248
; CURRENT APPLICATION NUMBER: US/09/898,556A
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 28
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-28

Query Match
Best Local Similarity 100.0%; Score 20; DB 9; Length 20;
Pred. No. 1.4e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 644 GGGAGAAGACTCCAGACTCC 663
Db 20 GGGAGAAGACTCCAGACTCC 1

RESULT 40
US-09-898-556A-29/c
; Sequence 29, Application US/09898556A
; Publication No. US20030087849A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKR1 EXPRESSION
; FILE REFERENCE: RTS-0248
; CURRENT APPLICATION NUMBER: US/09/898,556A
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 29
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-29

Query Match
Best Local Similarity 100.0%; Score 20; DB 9; Length 20;
Pred. No. 1.4e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 654 TCCAGACTCCTGTTGGAG 673
Db 20 TCCAGACTCCTGTTGGAG 1

RESULT 41
US-09-898-556A-30/c
; Sequence 30, Application US/09898556A
; Publication No. US20030087849A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKR1 EXPRESSION
; FILE REFERENCE: RTS-0248
; CURRENT APPLICATION NUMBER: US/09/898,556A
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 30
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-30

Query Match
0.7%; Score 20; DB 9; Length 20;
Score 20; DB 9; Length 20;
```

```

Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 680 CAAAATGGCAGCTTCAAGC 699
Db 20 CAAAATGGCAGCTTCAAGC 1

RESULT 42
US-09-898-556A-31/c
; Sequence 31, Application US/09898556A
; Publication No. US20030087849A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKR1 EXPRESSION
; FILE REFERENCE: RTS-0248
; CURRENT APPLICATION NUMBER: US/09/898,556A
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 31
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-31

Query Match
0.7%; Score 20; DB 9; Length 20;
Pred. No. 1.4e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 685 ATGCACCTTCAAGCAGCTT 704
Db 20 ATGCACCTTCAAGCAGCTT 1

RESULT 43
US-09-898-556A-32/c
; Sequence 32, Application US/09898556A
; Publication No. US20030087849A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKR1 EXPRESSION
; FILE REFERENCE: RTS-0248
; CURRENT APPLICATION NUMBER: US/09/898,556A
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 32
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-32

Query Match
0.7%; Score 20; DB 9; Length 20;
Pred. No. 1.4e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 720 GAACAAGCCAGCAGCAGTC 739
Db 20 GAACAAGCCAGCAGCAGTC 1

RESULT 44
US-09-898-556A-33/c
; Sequence 33, Application US/09898556A
; Publication No. US20030087849A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
```



```
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKRI EXPRESSION
; FILE REFERENCE: RTS-0248
; CURRENT APPLICATION NUMBER: US/09/898,556A
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 33
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-33

Query Match
Best Local Similarity 100.0%; Score 20; DB 9; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 732 GCACAGTCCAGGAAGACAA 751
DB 20 GCACAGTCCAGGAAGACAA 1

RESULT 45
US-09-898-556A-34/c
; Sequence 34, Application US/09898556A
; Publication No. US20030087849A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKRI EXPRESSION
; FILE REFERENCE: RTS-0248
; CURRENT APPLICATION NUMBER: US/09/898,556A
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 34
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-34

Query Match
Best Local Similarity 100.0%; Score 20; DB 9; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 751 ACACAGTGTGATATAGG 770
DB 20 ACACAGTGTGATATAGG 1

RESULT 46
US-09-898-556A-35/c
; Sequence 35, Application US/09898556A
; Publication No. US20030087849A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKRI EXPRESSION
; FILE REFERENCE: RTS-0248
; CURRENT APPLICATION NUMBER: US/09/898,556A
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-35

Query Match
Best Local Similarity 100.0%; Score 20; DB 9; Length 20;
```

```
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 760 TGGATATAGGTCAGCCCT 779
DB 20 TGGATATAGGTCAGCCCT 1

RESULT 47
US-09-898-556A-36/c
; Sequence 36, Application US/09898556A
; Publication No. US20030087849A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKRI EXPRESSION
; FILE REFERENCE: RTS-0248
; CURRENT APPLICATION NUMBER: US/09/898,556A
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 36
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-36

Query Match
Best Local Similarity 100.0%; Score 20; DB 9; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 788 GGCAGATCTAGAGGAACAG 807
DB 20 GGCAGATCTAGAGGAACAG 1

RESULT 48
US-09-898-556A-37/c
; Sequence 37, Application US/09898556A
; Publication No. US20030087849A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKRI EXPRESSION
; FILE REFERENCE: RTS-0248
; CURRENT APPLICATION NUMBER: US/09/898,556A
; CURRENT FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 37
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-37

Query Match
Best Local Similarity 100.0%; Score 20; DB 9; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 866 TGGCGCAGCCTTATCAAG 885
DB 20 TGGCGCAGCCTTATCAAG 1

RESULT 49
US-09-898-556A-38/c
; Sequence 38, Application US/09898556A
; Publication No. US20030087849A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF HKRI EXPRESSION
```

FILE REFERENCE: RTS-0248
CURRENT APPLICATION NUMBER: US/09/898,556A
CURRENT FILING DATE: 2001-07-03
NUMBER OF SEQ ID NOS: 89
SEQ ID NO: 38
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-38

Query Match 0.7%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 878 TATCAAGAGTCAACCTCC 897
DB 20 TATCAAGAGTCAACCTCC 1

RESULT 50
US-09-898-556A-39/C
Sequence 39, Application US/09898556A
Publication No. US20030087849A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
TITLE OF INVENTION: ANTISENSE MODULATION OF HKR1 EXPRESSION
FILE REFERENCE: RTS-0248
CURRENT APPLICATION NUMBER: US/09/898,556A
CURRENT FILING DATE: 2001-07-03
NUMBER OF SEQ ID NOS: 89
SEQ ID NO: 39
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-898-556A-39

Query Match 0.7%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 907 AGAAGACACAACCTGGGAG 926
DB 20 AGAAGACACAACCTGGGAG 1

Search completed: June 4, 2003, 12:47:08
Job time : 411 secs

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OM nucleic - nucleic search, using sw model

Run on: June 4, 2003, 07:24:51 ; Search time 132 seconds
(without alignments)
6440.212 Million cell updates/sec

Title: US-09-898-556A-3
Perfect score: 2772
Sequence: 1 caggcgcttaagctgttg.....ttctaccatctcaccct 2772

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 635134

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Issued Patents -NA:*

- 1: /cgn2-6/ptodata/1/ina/5A.COMB.seq:*
- 2: /cgn2-6/ptodata/1/ina/5B.COMB.seq:*
- 3: /cgn2-6/ptodata/1/ina/6A.COMB.seq:*
- 4: /cgn2-6/ptodata/1/ina/6B.COMB.seq:*
- 5: /cgn2-6/ptodata/1/ina/PTUS.COMB.seq:*
- 6: /cgn2-6/ptodata/1/ina/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	21.6	0.8	41	1	US-08-294-42A-6
C 2	21	0.8	50	3	US-08-388-029A-30
C 3	21	0.8	52	4	US-08-906-156A-72
C 4	21	0.8	59	4	US-08-952-793-236
C 5	21	0.8	59	5	PCT-US96-09455A-236
C 6	20.8	0.8	48	2	US-08-369-829A-7
C 7	20.8	0.8	48	2	US-08-586-676E-11
C 8	20.6	0.7	47	4	US-09-641-638-1290
C 9	20.6	0.7	52	4	US-08-952-793-244
C 10	20.6	0.7	52	5	PCT-US96-09455A-244
C 11	20.2	0.7	50	1	US-08-374-641-40
C 12	20.2	0.7	52	2	US-08-553-619B-13
C 13	20.2	0.7	53	1	US-08-242-035A-2
C 14	20.2	0.7	60	1	US-08-477-270-21
C 15	20	0.7	48	1	US-08-758-626-23
C 16	20	0.7	48	5	PCT-US94-07684-23
C 17	20	0.7	55	1	US-08-173-968-7
C 18	20	0.7	55	3	US-07-801-814D-7
C 19	19.8	0.7	47	3	US-08-726-807B-21
C 20	19.8	0.7	47	3	US-09-258-367-21
C 21	19.8	0.7	47	4	US-09-546-550-21
C 22	19.8	0.7	47	4	US-09-431-414-21
C 23	19.8	0.7	47	4	US-09-225-670-21
C 24	19.8	0.7	47	4	US-09-431-349C-21
C 25	19.8	0.7	57	3	US-08-863-813A-47
C 26	19.8	0.7	59	4	US-09-037-990B-60
C 27	19.6	0.7	56	1	US-08-461-184-9

C 28	19.6	0.7	56	1	US-08-463-675-9	Sequence 9, Appli
C 29	19.6	0.7	56	1	US-08-464-589-9	Sequence 9, Appli
C 30	19.6	0.7	60	4	US-08-406-030A-8	Sequence 8, Appli
C 31	19.6	0.7	60	4	US-08-406-030A-9	Sequence 9, Appli
C 32	19.4	0.7	33	4	US-08-169-715-14	Sequence 14, Appli
C 33	19.4	0.7	43	2	US-08-417-210A-99	Sequence 99, Appli
C 34	19.4	0.7	47	4	US-09-641-638-760	Sequence 760, App
C 35	19.4	0.7	56	2	US-08-417-210A-106	Sequence 106, App
C 36	19.2	0.7	41	3	US-08-973-965-1	Sequence 1, Appli
C 37	19.2	0.7	44	3	US-08-444-818-229	Sequence 229, App
C 38	19.2	0.7	45	1	US-08-171-389-100	Sequence 100, App
C 39	19.2	0.7	45	1	US-08-123-936-100	Sequence 100, App
C 40	19.2	0.7	45	2	US-08-475-228A-100	Sequence 100, App
C 41	19.2	0.7	45	3	US-08-482-060A-100	Sequence 100, App
C 42	19.2	0.7	45	4	US-09-354-947-100	Sequence 100, App
C 43	19.2	0.7	45	5	PCT-US93-12388-100	Sequence 100, App
C 44	19.2	0.7	48	2	US-08-859-649-10	Sequence 10, Appli
C 45	19.2	0.7	48	4	US-08-207-861-10	Sequence 10, Appli
C 46	19.2	0.7	58	2	US-08-431-527A-6	Sequence 6, Appli
C 47	19.2	0.7	59	4	US-08-485-355B-53	Sequence 53, Appli
C 48	19.2	0.7	38	1	US-08-373-124A-185	Sequence 185, App
C 49	19	0.7	38	1	US-08-435-628-185	Sequence 185, App
C 50	19	0.7	46	4	US-09-609-816-13	Sequence 13, App
C 51	19	0.7	57	4	US-08-869-380-6	Sequence 6, Appli
C 52	19	0.7	57	5	PCT-US95-13552-17	Sequence 17, Appli
C 53	18.8	0.7	40	4	US-09-359-304B-34	Sequence 34, Appli
C 54	18.8	0.7	43	1	US-08-253-877C-34	Sequence 34, Appli
C 55	18.8	0.7	43	1	US-08-253-877C-35	Sequence 35, Appli
C 56	18.8	0.7	43	2	US-08-452-164A-34	Sequence 34, Appli
C 57	18.8	0.7	43	2	US-08-452-164A-35	Sequence 35, Appli
C 58	18.8	0.7	49	1	US-08-105-463-378	Sequence 378, App
C 59	18.8	0.7	49	1	US-08-709-209-378	Sequence 378, App
C 60	18.8	0.7	49	1	US-08-458-101-378	Sequence 378, App
C 61	18.8	0.7	49	2	US-08-619-362A-6	Sequence 6, Appli
C 62	18.8	0.7	54	1	US-08-227-688-3	Sequence 3, Appli
C 63	18.8	0.7	54	4	US-09-368-169-3	Sequence 3, Appli
C 64	18.8	0.7	54	4	US-09-424-620B-14	Sequence 14, Appli
C 65	18.8	0.7	60	6	5194596-31	Patent No. 5194596
C 66	18.6	0.7	60	6	5219739-36	Patent No. 5219739
C 67	18.6	0.7	25	4	US-09-150-766-6	Sequence 6, Appli
C 68	18.6	0.7	36	1	US-08-311-486C-288	Sequence 288, App
C 69	18.6	0.7	38	4	US-09-084-120-15	Sequence 15, Appli
C 70	18.6	0.7	42	2	US-08-627-151A-17	Sequence 17, Appli
C 71	18.6	0.7	47	4	US-08-569-147-17	Sequence 17, Appli
C 72	18.6	0.7	48	1	US-08-017-570-16	Sequence 16, Appli
C 73	18.6	0.7	48	1	US-08-471-426-16	Sequence 16, Appli
C 74	18.6	0.7	48	5	PCT-US94-01709-16	Sequence 16, Appli
C 75	18.6	0.7	57	2	US-08-149-097D-25	Sequence 25, Appli
C 76	18.4	0.7	31	4	US-09-248-588-18	Sequence 18, Appli
C 77	18.4	0.7	42	1	US-08-375-116A-39	Sequence 39, Appli
C 78	18.4	0.7	42	4	US-09-250-580-4	Sequence 4, Appli
C 79	18.4	0.7	45	4	US-09-291-902-3	Sequence 3, Appli
C 80	18.4	0.7	45	1	US-08-222-177A-361	Sequence 361, App
C 81	18.4	0.7	49	1	US-08-486-137-4	Sequence 4, Appli
C 82	18.4	0.7	50	1	US-08-485-180-4	Sequence 4, Appli
C 83	18.4	0.7	50	1	US-08-419-765-4	Sequence 4, Appli
C 84	18.4	0.7	51	2	US-08-704-682-2	Sequence 2, Appli
C 85	18.4	0.7	53	5	PCT-US92-09955-15	Sequence 15, Appli
C 86	18.4	0.7	54	2	US-08-448-418-70	Sequence 70, Appli
C 87	18.4	0.7	54	2	US-08-448-418-71	Sequence 71, Appli
C 88	18.2	0.7	34	2	US-08-765-782A-30	Sequence 30, Appli
C 89	18.2	0.7	34	3	US-08-921-100-30	Sequence 30, Appli
C 90	18.2	0.7	34	3	US-08-880-142-30	Sequence 30, Appli
C 91	18.2	0.7	34	3	US-08-902-201-30	Sequence 30, Appli
C 92	18.2	0.7	34	4	US-09-416-557-30	Sequence 30, Appli
C 93	18.2	0.7	42	2	US-08-658-665-135	Sequence 135, App
C 94	18.2	0.7	42	4	US-08-796-617-111	Sequence 111, App
C 95	18.2	0.7	42	4	US-09-085-273-135	Sequence 135, App
C 96	18.2	0.7	43	4	US-09-489-979-2	Sequence 2, Appli
C 97	18.2	0.7	47	4	US-08-976-183A-11	Sequence 11, Appli
C 98	18.2	0.7	48	4	US-08-952-793-194	Sequence 194, App
C 99	18.2	0.7	48	4	US-09-302-620B-68	Sequence 68, Appli
C 100	18.2	0.7	48	4	US-09-569-572C-24	Sequence 24, Appli

101	18.2	0.7	48	5	PCT-US96-09455A-194	Sequence 194, App	c 174	17.8	0.6	38	1	US-08-435-628-189	Sequence 189, App
102	18.2	0.7	50	1	US-08-207-901-41	Sequence 41, Appl	175	17.8	0.6	38	4	US-09-262-773-118	Sequence 118, Appl
103	18.2	0.7	50	4	US-09-315-886C-13	Sequence 13, Appl	176	17.8	0.6	43	1	US-08-560-313A-8	Sequence 8, Appl
c 104	18.2	0.7	51	4	US-09-330-245A-4	Sequence 4, Appl	177	17.8	0.6	43	1	US-08-611-155B-12	Sequence 12, Appl
105	18.2	0.7	59	2	US-08-308-887A-5	Sequence 5, Appl	178	17.8	0.6	43	2	US-08-916-120A-14	Sequence 14, Appl
106	18.2	0.7	59	3	US-08-881-094-5	Sequence 5, Appl	179	17.8	0.6	43	4	US-08-358-627E-2	Sequence 2, Appl
107	18.2	0.7	60	3	US-08-545-860D-74	Sequence 74, Appl	180	17.8	0.6	45	4	US-09-315-793-4	Sequence 4, Appl
108	18.2	0.7	60	3	US-08-658-136-26	Sequence 26, Appl	181	17.8	0.6	45	4	US-09-027-998A-5	Sequence 5, Appl
c 109	18.2	0.7	60	4	US-09-275-850-277	Sequence 277, App	182	17.8	0.6	45	4	US-09-020-846-58	Sequence 58, Appl
c 110	18.2	0.7	60	4	US-08-290-736C-29	Sequence 29, Appl	183	17.8	0.6	45	4	US-08-028-84C-2	Sequence 2, Appl
c 111	18.2	0.7	60	5	PCT-US94-04496-74	Sequence 74, Appl	184	17.8	0.6	45	4	US-08-465-712C-2	Sequence 2, Appl
c 112	18	0.6	35	2	US-07-832-905B-24	Sequence 24, Appl	185	17.8	0.6	47	1	US-09-552-733-2	Sequence 2, Appl
c 113	18	0.6	35	2	US-08-700-757-24	Sequence 24, Appl	186	17.8	0.6	47	1	US-08-296-880-6	Sequence 6, Appl
c 114	18	0.6	36	1	US-08-170-588-1	Sequence 1, Appl	187	17.8	0.6	47	1	US-08-447-174A-6	Sequence 6, Appl
c 115	18	0.6	36	2	US-08-482-182-1	Sequence 1, Appl	c 187	17.8	0.6	47	1	US-08-434-743-1	Sequence 1, Appl
c 116	18	0.6	36	2	US-08-482-182-19	Sequence 19, Appl	c 188	17.8	0.6	47	1	US-08-685-793-1	Sequence 1, Appl
c 117	18	0.6	36	2	US-08-482-182-25	Sequence 25, Appl	c 189	17.8	0.6	47	1	US-08-685-793-8	Sequence 8, Appl
c 118	18	0.6	37	1	US-07-744-283C-43	Sequence 43, Appl	c 190	17.8	0.6	47	2	US-08-685-793-8	Sequence 8, Appl
c 119	18	0.6	37	5	PCT-US92-06821A-86	Sequence 86, Appl	c 191	17.8	0.6	47	3	US-08-800-641-6	Sequence 6, Appl
c 120	18	0.6	43	1	US-08-041-538-11	Sequence 11, Appl	c 192	17.8	0.6	47	4	US-09-613-263-3	Sequence 3, Appl
c 121	18	0.6	43	1	US-08-463-642-11	Sequence 11, Appl	c 193	17.8	0.6	47	4	US-09-613-263-3	Sequence 3, Appl
c 122	18	0.6	43	1	US-08-455-602-11	Sequence 11, Appl	c 194	17.8	0.6	49	4	US-09-358-972-117	Sequence 117, App
c 123	18	0.6	43	5	US-08-465-157-11	Sequence 11, Appl	c 195	17.8	0.6	49	4	US-09-358-972-118	Sequence 118, App
c 124	18	0.6	43	5	PCT-US91-05177-9	Sequence 9, Appl	c 196	17.8	0.6	49	4	US-09-383-316-16	Sequence 16, App
c 125	18	0.6	43	5	PCT-US91-09422-11	Sequence 11, Appl	c 197	17.8	0.6	49	4	US-09-383-316-17	Sequence 17, App
c 126	18	0.6	45	1	US-08-171-389-296	Sequence 296, App	c 198	17.8	0.6	49	4	US-09-609-816-14	Sequence 14, Appl
c 127	18	0.6	45	1	US-08-233-009-43	Sequence 43, Appl	c 199	17.8	0.6	50	2	US-08-867-579-1	Sequence 1, Appl
c 128	18	0.6	45	1	US-08-123-936-296	Sequence 296, App	c 200	17.8	0.6	51	4	US-09-460-303-4	Sequence 4, Appl
c 129	18	0.6	45	2	US-08-475-228A-296	Sequence 296, App	c 201	17.8	0.6	52	4	US-09-506-729-11	Sequence 11, Appl
c 130	18	0.6	45	3	US-08-482-080A-296	Sequence 296, App	c 202	17.8	0.6	53	4	US-09-275-850-267	Sequence 267, App
c 131	18	0.6	45	4	US-09-354-947-296	Sequence 296, App	c 203	17.8	0.6	53	4	US-09-275-850-269	Sequence 269, App
c 132	18	0.6	45	5	PCT-US93-12368-296	Sequence 296, App	c 204	17.8	0.6	53	4	US-09-813-781-89	Sequence 89, Appl
c 133	18	0.6	46	4	US-09-380-190A-63	Sequence 63, Appl	c 205	17.8	0.6	54	1	US-08-081-539-57	Sequence 57, Appl
c 134	18	0.6	47	4	US-09-641-638-769	Sequence 769, Appl	c 206	17.8	0.6	54	1	US-08-466-647-57	Sequence 57, Appl
c 135	18	0.6	48	2	US-09-641-638-1113	Sequence 1113, App	c 207	17.8	0.6	54	1	US-08-828-323-12	Sequence 12, Appl
c 136	18	0.6	48	2	US-08-477-553A-13	Sequence 13, Appl	c 208	17.8	0.6	54	1	US-08-279-058B-12	Sequence 12, Appl
c 137	18	0.6	49	1	US-08-483-883-72	Sequence 72, Appl	c 209	17.8	0.6	54	1	US-08-279-594-13	Sequence 13, Appl
c 138	18	0.6	49	1	US-08-483-883-72	Sequence 72, Appl	c 210	17.8	0.6	54	1	US-08-311-486C-14	Sequence 14, Appl
c 139	18	0.6	49	2	US-08-484-993B-57	Sequence 57, Appl	c 211	17.8	0.6	54	2	US-08-773-293-24	Sequence 24, Appl
c 140	18	0.6	49	2	US-08-487-113D-72	Sequence 72, Appl	c 212	17.8	0.6	54	3	US-09-098-293-24	Sequence 24, Appl
c 141	18	0.6	49	2	US-08-473-503-72	Sequence 72, Appl	c 213	17.8	0.6	54	3	US-09-094-919-13	Sequence 13, Appl
c 142	18	0.6	49	2	US-08-483-933-72	Sequence 72, Appl	c 214	17.8	0.6	54	4	US-09-506-729-17	Sequence 17, App
c 143	18	0.6	49	2	US-08-484-158B-57	Sequence 57, Appl	c 215	17.8	0.6	54	4	US-08-828-323-12	Sequence 12, Appl
c 144	18	0.6	49	2	US-08-484-596A-57	Sequence 57, Appl	c 216	17.8	0.6	54	4	US-09-438-954-29	Sequence 29, Appl
c 145	18	0.6	49	2	US-08-480-150A-57	Sequence 57, Appl	c 217	17.8	0.6	57	1	US-08-530-492-107	Sequence 107, App
c 146	18	0.6	49	2	US-08-720-420A-72	Sequence 72, Appl	c 218	17.8	0.6	57	4	US-08-906-517-107	Sequence 107, App
c 147	18	0.6	49	3	US-08-458-731-57	Sequence 57, Appl	c 219	17.8	0.6	58	1	US-08-076-094A-9	Sequence 9, Appl
c 148	18	0.6	49	3	US-08-149-223A-57	Sequence 57, Appl	c 220	17.8	0.6	58	4	US-09-439-897-42	Sequence 42, Appl
c 149	18	0.6	49	3	US-08-714-017-72	Sequence 72, Appl	c 221	17.8	0.6	58	5	PCT-US94-06132-9	Sequence 9, Appl
c 150	18	0.6	49	3	US-08-475-660-72	Sequence 72, Appl	c 222	17.8	0.6	59	2	US-08-704-473-23	Sequence 23, Appl
c 151	18	0.6	51	3	US-08-930-503A-14	Sequence 14, Appl	c 223	17.8	0.6	60	3	US-08-658-136-24	Sequence 24, Appl
c 152	18	0.6	52	2	US-08-560-098A-41	Sequence 41, Appl	c 224	17.6	0.6	27	4	US-08-584-040-278	Sequence 278, App
c 153	18	0.6	53	3	US-08-864-473-60	Sequence 60, Appl	c 225	17.6	0.6	28	1	US-07-316-902-3	Sequence 3, Appl
c 154	18	0.6	53	4	US-09-440-523-60	Sequence 60, Appl	c 226	17.6	0.6	35	1	US-08-317-432A-34	Sequence 34, Appl
c 155	18	0.6	54	2	US-08-588-201-11	Sequence 11, Appl	c 227	17.6	0.6	35	4	US-08-646-301A-5	Sequence 5, Appl
c 156	18	0.6	54	2	US-09-169-605-11	Sequence 11, Appl	c 228	17.6	0.6	35	4	US-08-481-968A-9	Sequence 9, Appl
c 157	18	0.6	54	3	US-08-893-327-11	Sequence 11, Appl	c 229	17.6	0.6	35	4	US-08-154-712B-9	Sequence 9, Appl
c 158	18	0.6	54	4	US-08-706-945D-69	Sequence 69, Appl	c 230	17.6	0.6	36	1	US-07-781-254A-27	Sequence 27, Appl
c 159	18	0.6	55	2	US-08-774-065-8	Sequence 8, Appl	c 231	17.6	0.6	36	1	US-08-311-760A-91	Sequence 91, Appl
c 160	18	0.6	55	2	US-07-609-716-72	Sequence 72, Appl	c 232	17.6	0.6	36	2	US-08-441-887A-7	Sequence 7, Appl
c 161	18	0.6	60	3	US-08-475-411A-72	Sequence 72, Appl	c 233	17.6	0.6	36	2	US-08-585-664B-1864	Sequence 1864, App
c 162	18	0.6	60	4	US-08-478-029A-72	Sequence 72, Appl	c 234	17.6	0.6	36	2	US-08-774-310-91	Sequence 91, Appl
c 163	18	0.6	60	4	US-09-275-850-256	Sequence 256, App	c 235	17.6	0.6	36	3	US-08-544-381B-113	Sequence 113, App
c 164	18	0.6	60	4	US-09-218-089A-26	Sequence 26, Appl	c 236	17.6	0.6	36	4	US-09-038-073-1864	Sequence 1864, App
c 165	17.8	0.6	22	4	US-07-963-475-6	Sequence 6, Appl	c 237	17.6	0.6	37	4	US-07-875-790B-11	Sequence 11, Appl
c 166	17.8	0.6	30	1	US-09-289-368-2	Sequence 2, Appl	c 238	17.6	0.6	39	4	US-09-281-481A-11	Sequence 11, Appl
c 167	17.8	0.6	30	1	US-08-186-229-47	Sequence 47, Appl	c 239	17.6	0.6	41	1	US-08-294-424-20	Sequence 20, Appl
c 168	17.8	0.6	30	2	US-08-470-124-47	Sequence 47, Appl	c 240	17.6	0.6	42	4	US-09-382-616A-25	Sequence 25, Appl
c 169	17.8	0.6	30	4	US-09-129-686-8	Sequence 8, Appl	c 241	17.6	0.6	43	2	US-08-756-506-19	Sequence 19, Appl
c 170	17.8	0.6	32	4	US-09-566-581-8	Sequence 8, Appl	c 242	17.6	0.6	43	4	US-08-057-430A-9	Sequence 9, Appl
c 171	17.8	0.6	38	1	US-08-373-124A-177	Sequence 177, App	c 243	17.6	0.6	45	1	US-08-171-389-185	Sequence 185, App
c 172	17.8	0.6	38	1	US-08-373-124A-189	Sequence 189, App	c 244	17.6	0.6	45	1	US-08-123-936-185	Sequence 185, App
c 173	17.8	0.6	38	1	US-08-435-628-177	Sequence 177, App	c 245	17.6	0.6	45	1	US-08-253-877C-37	Sequence 37, Appl

247	17.6	0.6	45	2	US-08-475-228A-185	Sequence 185, App	C 320	17.4	0.6	47	3	US-08-482-080A-4	Sequence 4, Appl
248	17.6	0.6	45	2	US-08-452-164A-37	Sequence 37, Appl	C 321	17.4	0.6	47	4	US-09-349-644-8	Sequence 8, Appl
249	17.6	0.6	45	3	US-08-482-080A-185	Sequence 185, App	C 322	17.4	0.6	47	4	US-09-354-947-4	Sequence 8, Appl
250	17.6	0.6	45	3	US-08-864-473-70	Sequence 70, Appl	C 323	17.4	0.6	47	4	US-09-641-638-820	Sequence 820, Appl
251	17.6	0.6	45	4	US-09-440-523-70	Sequence 70, Appl	C 324	17.4	0.6	47	4	US-09-641-638-1264	Sequence 1264, Ap
C 252	17.6	0.6	45	4	US-09-069-821-23	Sequence 23, Appl	C 325	17.4	0.6	49	5	PCT-US93-12388-4	Sequence 4, Appl
253	17.6	0.6	45	4	US-09-354-947-185	Sequence 185, App	C 326	17.4	0.6	49	5	US-08-706-135-5	Sequence 5, Appl
254	17.6	0.6	45	5	PCT-US93-12388-185	Sequence 185, App	C 327	17.4	0.6	49	5	PCT-US95-16904-5	Sequence 5, Appl
C 255	17.6	0.6	46	5	PCT-US95-11684-24	Sequence 24, Appl	C 328	17.4	0.6	52	1	US-08-301-872A-11	Sequence 11, Appl
256	17.6	0.6	47	1	US-08-222-177A-458	Sequence 458, App	C 329	17.4	0.6	52	1	US-08-301-872A-11	Sequence 11, Appl
257	17.6	0.6	47	1	US-09-641-638-1167	Sequence 1167, Ap	C 330	17.4	0.6	52	2	US-08-443-372A-11	Sequence 11, Appl
C 258	17.6	0.6	49	2	US-08-756-506-18	Sequence 18, Appl	C 331	17.4	0.6	52	2	US-08-443-372A-11	Sequence 11, Appl
C 259	17.6	0.6	49	4	US-08-849-567A-69	Sequence 69, Appl	C 332	17.4	0.6	52	2	US-08-770-235A-55	Sequence 65, Appl
260	17.6	0.6	50	1	US-09-206-942-95	Sequence 95, Appl	C 333	17.4	0.6	53	1	US-08-429-181-12	Sequence 12, Appl
C 261	17.6	0.6	50	4	US-08-207-901-78	Sequence 78, Appl	C 334	17.4	0.6	53	1	US-08-164-388-12	Sequence 12, Appl
C 262	17.6	0.6	50	2	US-08-860-174A-22	Sequence 22, Appl	C 335	17.4	0.6	54	2	US-08-446-418-72	Sequence 72, Appl
C 263	17.6	0.6	50	4	US-08-646-695-10	Sequence 10, Appl	C 336	17.4	0.6	57	1	US-07-911-531-12	Sequence 12, Appl
C 264	17.6	0.6	50	4	US-09-171-025-21	Sequence 21, Appl	C 337	17.4	0.6	57	1	US-07-693-636A-12	Sequence 12, Appl
C 265	17.6	0.6	50	4	US-08-906-156A-71	Sequence 71, Appl	C 338	17.4	0.6	57	3	US-09-159-274-1	Sequence 1, Appl
C 266	17.6	0.6	50	5	PCT-US95-13975-59	Sequence 59, Appl	C 339	17.4	0.6	57	4	US-09-461-697-147	Sequence 147, App
267	17.6	0.6	50	5	PCT-US96-06053-10	Sequence 10, Appl	C 340	17.4	0.6	57	4	US-09-238-356-7	Sequence 7, Appl
C 268	17.6	0.6	51	1	US-08-208-886C-52	Sequence 52, Appl	C 341	17.4	0.6	58	1	US-08-332-420-47	Sequence 47, Appl
C 269	17.6	0.6	51	1	US-08-704-744-52	Sequence 52, Appl	C 342	17.4	0.6	58	2	US-08-467-948A-18	Sequence 18, Appl
C 270	17.6	0.6	51	2	US-08-469-357-52	Sequence 52, Appl	C 343	17.4	0.6	59	4	US-08-467-947A-18	Sequence 18, Appl
C 271	17.6	0.6	51	2	US-08-290-793B-52	Sequence 52, Appl	C 344	17.4	0.6	59	4	US-09-508-277C-9	Sequence 9, Appl
C 272	17.6	0.6	51	3	US-08-284-516C-26	Sequence 26, Appl	C 345	17.4	0.6	60	3	US-08-545-860D-73	Sequence 73, Appl
C 273	17.6	0.6	51	4	US-09-537-911A-26	Sequence 26, Appl	C 346	17.4	0.6	60	3	US-08-643-704A-9	Sequence 9, Appl
274	17.6	0.6	53	4	US-09-710-200-13	Sequence 13, Appl	C 347	17.4	0.6	60	4	US-09-502-558-16	Sequence 16, Appl
C 275	17.6	0.6	55	4	US-09-423-439-12	Sequence 12, Appl	C 348	17.4	0.6	60	5	PCT-US94-04496-73	Sequence 73, Appl
276	17.6	0.6	55	5	PCT-US92-10024-8	Sequence 8, Appl	C 349	17.2	0.6	24	4	US-08-943-731-509	Sequence 509, App
C 277	17.6	0.6	58	2	US-08-431-527A-7	Sequence 7, Appl	C 350	17.2	0.6	25	4	US-09-183-412-39	Sequence 39, Appl
C 278	17.6	0.6	60	2	US-08-053-451B-121	Sequence 121, App	C 351	17.2	0.6	25	4	US-09-150-766-5	Sequence 5, Appl
279	17.6	0.6	60	3	US-08-911-894-64	Sequence 64, Appl	C 352	17.2	0.6	28	1	US-08-318-867A-19	Sequence 19, Appl
C 280	17.6	0.6	60	3	US-08-754-681-19	Sequence 19, Appl	C 353	17.2	0.6	30	1	US-08-952-088A-5	Sequence 5, Appl
C 281	17.6	0.6	60	4	US-09-357-487B-19	Sequence 19, Appl	C 354	17.2	0.6	30	1	US-08-186-223-38	Sequence 38, Appl
282	17.6	0.6	60	4	US-09-602-428-19	Sequence 19, Appl	C 355	17.2	0.6	30	2	US-08-244-466-1	Sequence 1, Appl
C 283	17.6	0.6	60	5	PCT-US96-03916-49	Sequence 49, Appl	C 356	17.2	0.6	30	2	US-08-470-121-38	Sequence 38, Appl
C 284	17.4	0.6	32	1	US-07-618-312A-6	Sequence 6, Appl	C 357	17.2	0.6	30	2	US-08-629-001A-116	Sequence 116, App
C 285	17.4	0.6	32	1	US-08-280-228-6	Sequence 6, Appl	C 358	17.2	0.6	30	4	US-08-642-274D-195	Sequence 195, App
C 286	17.4	0.6	36	1	US-08-291-932A-516	Sequence 516, App	C 359	17.2	0.6	33	1	US-08-292-945-1	Sequence 1, Appl
C 287	17.4	0.6	36	2	US-08-292-620A-1408	Sequence 1408, Ap	C 360	17.2	0.6	33	1	US-08-252-073A-1	Sequence 1, Appl
C 288	17.4	0.6	36	2	US-08-292-620A-1505	Sequence 1505, Ap	C 361	17.2	0.6	33	5	PCT-US93-12074-1	Sequence 1, Appl
C 289	17.4	0.6	36	2	US-08-585-684B-1559	Sequence 1559, Ap	C 362	17.2	0.6	34	2	US-08-734-591A-94	Sequence 94, Appl
C 290	17.4	0.6	36	3	US-09-071-845-1408	Sequence 1408, Ap	C 363	17.2	0.6	34	3	US-08-470-335-94	Sequence 94, Appl
C 291	17.4	0.6	36	3	US-09-071-845-1505	Sequence 1505, Ap	C 364	17.2	0.6	34	4	US-08-734-664A-94	Sequence 94, Appl
C 292	17.4	0.6	36	4	US-09-038-073-1559	Sequence 1559, Ap	C 365	17.2	0.6	34	4	US-08-470-339-94	Sequence 94, Appl
C 293	17.4	0.6	37	1	US-08-273-362-1	Sequence 1, Appl	C 366	17.2	0.6	34	4	US-08-973-131-67	Sequence 67, Appl
C 294	17.4	0.6	37	3	US-08-702-870A-17	Sequence 17, Appl	C 367	17.2	0.6	34	4	US-08-467-602-94	Sequence 94, Appl
C 295	17.4	0.6	38	1	US-08-373-124A-181	Sequence 181, App	C 368	17.2	0.6	36	2	US-08-436-065-7	Sequence 7, Appl
C 296	17.4	0.6	38	1	US-08-435-628-181	Sequence 181, App	C 369	17.2	0.6	36	2	US-08-585-585A-13	Sequence 13, Appl
C 297	17.4	0.6	41	4	US-08-962-281-18	Sequence 18, Appl	C 370	17.2	0.6	36	3	US-08-685-808-12	Sequence 12, Appl
298	17.4	0.6	42	1	US-07-981-525-12	Sequence 12, Appl	C 371	17.2	0.6	36	4	US-08-505-860C-12	Sequence 12, Appl
C 299	17.4	0.6	42	1	US-08-220-033-12	Sequence 12, Appl	C 372	17.2	0.6	38	1	US-08-373-124A-197	Sequence 197, App
300	17.4	0.6	42	2	US-08-465-491-12	Sequence 12, Appl	C 373	17.2	0.6	38	1	US-08-373-124A-1384	Sequence 1384, Ap
301	17.4	0.6	42	2	US-08-986-617-12	Sequence 12, Appl	C 374	17.2	0.6	38	1	US-08-599-252-74	Sequence 74, Appl
302	17.4	0.6	42	3	US-08-813-507-131	Sequence 131, App	C 375	17.2	0.6	38	1	US-08-436-074-47	Sequence 47, Appl
303	17.4	0.6	42	4	US-09-290-577-8	Sequence 8, Appl	C 376	17.2	0.6	38	1	US-08-435-628-197	Sequence 197, App
C 304	17.4	0.6	42	4	US-09-290-577-9	Sequence 9, Appl	C 377	17.2	0.6	38	1	US-08-435-628-184	Sequence 184, Ap
305	17.4	0.6	42	4	US-09-290-452-8	Sequence 8, Appl	C 378	17.2	0.6	38	5	PCT-US96-06332-74	Sequence 74, Appl
306	17.4	0.6	42	4	US-09-290-452-9	Sequence 9, Appl	C 379	17.2	0.6	39	2	PCT-US96-06583-74	Sequence 74, Appl
307	17.4	0.6	42	4	US-09-290-338-8	Sequence 8, Appl	C 380	17.2	0.6	39	5	US-08-455-968E-44	Sequence 44, Appl
308	17.4	0.6	42	4	US-09-290-338-9	Sequence 9, Appl	C 381	17.2	0.6	39	4	US-09-262-777-74	Sequence 74, Appl
C 309	17.4	0.6	42	4	US-09-464-453-131	Sequence 131, App	C 382	17.2	0.6	44	1	US-08-153-071-6	Sequence 6, Appl
C 310	17.4	0.6	43	4	US-09-117-860-44	Sequence 44, Appl	C 383	17.2	0.6	44	1	US-08-609-271-13	Sequence 13, Appl
311	17.4	0.6	43	4	US-09-117-860-46	Sequence 46, Appl	C 384	17.2	0.6	44	2	US-08-438-511-6	Sequence 6, Appl
312	17.4	0.6	45	2	US-08-495-695B-20	Sequence 20, Appl	C 385	17.2	0.6	44	2	US-08-487-431-9	Sequence 9, Appl
C 313	17.4	0.6	45	5	PCT-US94-14436-20	Sequence 20, Appl	C 386	17.2	0.6	44	3	US-08-188-374-13	Sequence 13, Appl
C 314	17.4	0.6	46	1	US-08-343-682-3	Sequence 3, Appl	C 387	17.2	0.6	44	3	US-08-973-629-9	Sequence 9, Appl
C 315	17.4	0.6	46	1	US-08-343-682-6	Sequence 6, Appl	C 388	17.2	0.6	45	1	US-08-291-1059-4	Sequence 4, Appl
C 316	17.4	0.6	46	2	US-08-652-558-28	Sequence 28, Appl	C 389	17.2	0.6	45	5	PCT-US95-10579-4	Sequence 4, Appl
C 317	17.4	0.6	47	1	US-08-171-389-4	Sequence 4, Appl	C 390	17.2	0.6	46	1	US-08-271-880A-90	Sequence 90, Appl
C 318	17.4	0.6	47	1	US-08-123-936-4	Sequence 4, Appl	C 391	17.2	0.6	46	1	US-08-271-880A-113	Sequence 113, App
C 319	17.4	0.6	47	2	US-08-475-228A-4	Sequence 4, Appl	C 392	17.2	0.6	46	2	US-08-910-408-90	Sequence 90, Appl

C 393	17.2	0.6	46	2	US-08-910-408-11.3
C 394	17.2	0.6	46	3	US-08-803-088-19
C 395	17.2	0.6	46	3	US-09-249-213-90
C 396	17.2	0.6	46	3	US-09-249-215-11.3
C 397	17.2	0.6	47	1	US-08-171-389-23.7
C 398	17.2	0.6	47	1	US-08-123-936-23.7
C 399	17.2	0.6	47	2	US-08-475-228A-73
C 400	17.2	0.6	47	2	US-08-771-624B-16
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C 402	17.2	0.6	47	3	US-08-482-080A-23
C 403	17.2	0.6	47	4	US-09-354-947-23.7
C 404	17.2	0.6	47	4	US-09-641-638-95.2
C 405	17.2	0.6	47	4	US-09-641-638-96.5
C 406	17.2	0.6	47	4	US-09-641-638-97.4
C 407	17.2	0.6	47	5	PCT-US93-12388-23
C 408	17.2	0.6	48	1	US-08-483-889-67
C 409	17.2	0.6	48	1	US-08-483-889-67
C 410	17.2	0.6	48	2	US-08-487-113D-67
C 411	17.2	0.6	48	2	US-08-473-503-67
C 412	17.2	0.6	48	2	US-08-483-932-67
C 413	17.2	0.6	48	2	US-08-720-420A-67
C 414	17.2	0.6	48	3	US-08-714-017-67
C 415	17.2	0.6	48	3	US-07-602-848E-13
C 416	17.2	0.6	48	3	US-08-475-680-67
C 417	17.2	0.6	49	1	US-08-198-670A-34
C 418	17.2	0.6	49	1	US-08-882-876-17
C 419	17.2	0.6	49	4	US-09-233-874A-17
C 420	17.2	0.6	50	1	US-07-828-444-6
C 421	17.2	0.6	50	1	US-08-171-389-55.8
C 422	17.2	0.6	50	1	US-08-384-708A-5
C 423	17.2	0.6	50	1	US-08-123-936-55.8
C 424	17.2	0.6	50	2	US-08-475-228A-55
C 425	17.2	0.6	50	3	US-08-482-080A-55
C 426	17.2	0.6	50	4	US-08-687-421-5
C 427	17.2	0.6	50	4	PCT-US93-12388-55
C 428	17.2	0.6	50	5	US-09-354-947-55.8
C 429	17.2	0.6	51	1	US-08-222-177A-33
C 430	17.2	0.6	52	2	US-08-828-876-68
C 431	17.2	0.6	52	4	US-08-943-136-19
C 432	17.2	0.6	52	4	US-09-973-518-19
C 433	17.2-	0.6	52	4	US-09-233-874A-68
C 434	17.2	0.6	53	1	US-08-429-181-40
C 435	17.2	0.6	53	1	US-08-164-388-40
C 436	17.2	0.6	54	4	US-08-797-812-5
C 437	17.2	0.6	55	4	US-09-357-740-18
C 438	17.2	0.6	57	4	US-08-129-722A-7
C 439	17.2	0.6	58	1	US-08-219-012-55
C 440	17.2	0.6	58	4	US-08-687-421-24.3
C 441	17.2	0.6	58	6	5422249-10
C 442	17.2	0.6	59	2	US-08-704-473-21
C 443	17.2	0.6	60	2	US-08-117-952-75.9
C 444	17.2	0.6	60	2	US-08-117-952-76.0
C 445	17.2	0.6	60	3	US-07-921-104D-25
C 446	17.2	0.6	60	3	US-09-023-228B-11.1
C 447	17.2	0.6	60	4	US-09-055-075C-7
C 448	17.2	0.6	60	4	US-09-055-075C-9
C 449	17.2	0.6	60	4	US-09-053-075C-11
C 450	17.2	0.6	60	4	US-09-163-025B-11
C 451	17.2	0.6	60	4	US-09-218-089A-11
C 452	17	0.6	27	4	US-08-584-040-16.8
C 453	17	0.6	29	3	US-09-033-055A-17
C 454	17	0.6	30	1	US-08-106-761-5
C 455	17	0.6	31	1	US-08-451-715A-53
C 456	17	0.6	31	1	US-08-311-486C-7.9
C 457	17	0.6	36		

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C 456	17	0.6	42	3	US-08-967-158-4	Sequence 4	Appl 1
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C 458	17	0.6	43	4	US-09-042-353-401	Sequence 401	Appl 1
C 459	17	0.6	43	4	US-08-758-417A-251	Sequence 251	Appl 1
C 470	17	0.6	44	2	US-08-331-389A-27	Sequence 27	Appl 1
C 471	17	0.6	44	2	US-08-790-963-86	Sequence 86	Appl 1
C 472	17	0.6	44	3	US-08-990-176A-2	Sequence 2	Appl 1
C 473	17	0.6	44	4	US-09-192-657A-27	Sequence 27	Appl 1
C 474	17	0.6	44	4	US-09-371-774-86	Sequence 86	Appl 1
C 475	17	0.6	45	1	US-08-337-268A-58	Sequence 58	Appl 1
C 476	17	0.6	45	1	US-08-484-570A-58	Sequence 58	Appl 1
C 477	17	0.6	45	2	US-08-882-756-1	Sequence 1	Appl 1
C 478	17	0.6	45	2	US-08-882-756-2	Sequence 2	Appl 1
C 479	17	0.6	45	2	US-08-882-756-5	Sequence 5	Appl 1
C 480	17	0.6	45	2	US-08-687-355A-12	Sequence 12	Appl 1
C 481	17	0.6	45	4	US-09-301-153-1	Sequence 1	Appl 1
C 482	17	0.6	45	4	US-09-301-153-2	Sequence 2	Appl 1
C 483	17	0.6	45	4	US-09-358-507-259	Sequence 259	Appl 1
C 484	17	0.6	45	4	US-09-218-207-259	Sequence 259	Appl 1
C 485	17	0.6	45	4	US-09-407-367-12	Sequence 12	Appl 1
C 486	17	0.6	46	4	US-08-977-378-19	Sequence 19	Appl 1
C 487	17	0.6	47	4	US-08-976-183A-10	Sequence 10	Appl 1
C 488	17	0.6	47	4	US-09-641-638-907	Sequence 907	Appl 1
C 489	17	0.6	47	4	US-09-641-638-1047	Sequence 1047	Appl 1
C 490	17	0.6	47	4	US-09-641-638-1080	Sequence 1080	Appl 1
C 491	17	0.6	48	2	US-08-618-911-10	Sequence 10	Appl 1
C 492	17	0.6	48	4	US-09-710-200-7	Sequence 7	Appl 1
C 493	17	0.6	48	4	US-09-518-914-23	Sequence 23	Appl 1
C 494	17	0.6	49	2	US-09-002-177-18	Sequence 18	Appl 1
C 495	17	0.6	49	4	US-09-374-584-18	Sequence 18	Appl 1
C 496	17	0.6	49	4	US-09-538-709-1004	Sequence 1004	Appl 1
C 497	17	0.6	50	4	US-08-974-691-14	Sequence 14	Appl 1
C 498	17	0.6	51	2	US-08-525-506-7	Sequence 7	Appl 1
C 499	17	0.6	51	4	US-09-085-028-7	Sequence 7	Appl 1
C 500	17	0.6	52	3	US-08-388-029A-31	Sequence 31	Appl 1

ALIGNMENTS

RESULT 1
US-08-294-424-6/c
; Sequence 6, Application US/08294424

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: GENERAL INFORMATION:
: APPLICANT: Vary, Calvin
: TITLE OF INVENTION: NUCLEIC ACID SEQUENCE DETECTION BY
: TITLE OF INVENTION: TRIPLE HELIX FORMATION
: NUMBER OF SEQUENCES: 49

```

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardso

STREET: 225 Franklin

CITY: BOSTON
STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READABLE

MEDIUM TYPE: 3.

COMPUTER: IBM
OPERATING SYSTEM:

SOFTWARE: WORD

CURRENT APPLICATIONS

APPLICATION NUMBER

CLASSIFICATION:

CHARACTERIZATION:
PRIOR APPLICATION

APPLICATION NUME

FILING DATE: 16

APPLICATION NUMBER

FILED DATE: 1/17/2009

NAME: Freeman,

REGISTRATION NUM.

REFERENCE/DOCKET NUMBER: 00088-037001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 41
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-294-424-6

Query Match 0.8%; Score 21.6; DB 1; Length 41;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 27; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 374 GCGAGGGAGAGCCCTGGAGAGAGAGAAAATG 409
Db 39 GCGTTGCTGATCGCTTGGAGAGAGAGAAAAG 4

RESULT 2
US-08-388-029A-30/C
Sequence 30, Application US/08388029A
Patent No. 6110665
GENERAL INFORMATION:
APPLICANT: FENGER, CLARA K.
APPLICANT: GRANSTROM, DAVID R.
APPLICANT: GAJADHAR, ALVIN A.
TITLE OF INVENTION: SARCOCYSTITIS NEURONA DIAGNOSTIC PRIMER
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER
STREET: 99 CANAL CENTER PLAZA, SUITE 300
CITY: ALEXANDRIA
STATE: VIRGINIA
COUNTRY: US
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,029A
FILING DATE: 14-FEB-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PRICE, ROBERT L.
REGISTRATION NUMBER: 22,685
REFERENCE/DOCKET NUMBER: 434-046
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
TELEX: AMERPAT
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-388-029A-30

Query Match 0.8%; Score 21; DB 3; Length 50;
Best Local Similarity 58.7%; Pred. No. 2.6e+03;
Matches 27; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1637 CCGGAATCAACCCGTGATCAGCGACAGAGACACTCAGGGGAG 1682
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Db 50 CCGGANCGAACCTTAATNCCCNNNACNNNACNCCAGCGGAG 5

RESULT 3
US-08-906-156A-72/C
Sequence 72, Application US/08906156A
Patent No. 6287854
GENERAL INFORMATION:
APPLICANT: SPURR, NIGEL K
APPLICANT: GRAY, IAN C
APPLICANT: STEWART, LORNA M
TITLE OF INVENTION: DIAGNOSIS OF SUSCEPTIBILITY TO CANCER
TITLE OF INVENTION: AND TREATMENT THEREOF
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHIE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,156A
FILING DATE: 05-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/042,655
FILING DATE: 02-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,147
FILING DATE: 13-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,840
FILING DATE: 23-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/96GB/02588
FILING DATE: 22-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 1090-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4100
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: human
US-08-906-156A-72

Query Match 0.8%; Score 21; DB 4; Length 52;
Best Local Similarity 82.8%; Pred. No. 2.6e+03;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 528 CTGTTTCAGAGTTTATGGGACAGGAATCC 556
Db 41 CTGCTTCAGAGCTTTCTGACAGGAATCC 13
||||| ||||||| | | | ||| || |||||

RESULT 4
US-08-952-793-236
Sequence 236, Application US/08952793

```

1 NUMBER OF SEQUENCES: 390
2 CORRESPONDENCE ADDRESS:
3 ADDRESSEE: Swanson & Bratschun, L.L.C.
4 STREET: 8400 E. Prentice Avenue, Suite 200
5 CITY: Englewood
6 STATE: Colorado
7 COUNTRY: USA
8 ZIP: 80111
9
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
12 COMPUTER: IBM pc compatible
13 OPERATING SYSTEM: MS-DOS
14 SOFTWARE: WordPerfect 6.0
15
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER: PCT/US96/09455A
18 FILING DATE: 05 JUNE 1996
19 CLASSIFICATION:
20
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: 08/479,724
23 FILING DATE: 07-JUNE-1995
24
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: 08/472,256
27 FILING DATE: 07-JUNE-1995
28
29 PRIOR APPLICATION DATA:
30 APPLICATION NUMBER: 08/472,255
31 FILING DATE: 07-JUNE-1995
32
33 PRIOR APPLICATION DATA:
34 APPLICATION NUMBER: 08/477,829
35 FILING DATE: 07-JUNE-1995
36
37 ATTORNEY/AGENT INFORMATION:
38 NAME: Barry J. Swanson
39
40 REGISTRATION NUMBER: 33,215
41 REFERENCE/DOCKET NUMBER: NEX40C/PCT
42 TELECOMMUNICATION INFORMATION:
43 TELEPHONE: (303) 793-3333
44 TELEFAX: (303) 793-3433
45
46 INFORMATION FOR SEQ. ID NO: 236:
47
48 SEQUENCE CHARACTERISTICS:
49 LENGTH: 59 base pairs
50 TYPE: nucleic acid
51 STRANDEDNESS: single
52 TOPOLOGY: linear
53
54 MOLECULE TYPE: RNA
55
56 FEATURE:
57
58 OTHER INFORMATION: All C's are 2'-F cytosine
59
60 FEATURE:
61
62 OTHER INFORMATION: All U's are 2'-F uracil
63
64 PCT-US96-09455A-236
65
66 Query Match 0.8%; Score 21; DB 5; length 59;
67 Best Local Similarity 62.2%; Pred. No. 2.9e+03;
68 Matches 28; Conservative 2; Mismatches 15; Indels 0; Gaps 0.
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COUNTRY: US
ZIP: 07936
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (Epo)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/369,829A
FILING DATE: 6-JAN-95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EPO 94810006.0
FILING DATE: 7-JAN-94
ATTORNEY/AGENT INFORMATION:
NAME: No. 5861377ak, Henry P.
REGISTRATION NUMBER: 33200
REFERENCE/DOCKET NUMBER: 4-19942/A/DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc.feature
LOCATION: 1..48
OTHER INFORMATION: /function= "synthetic oligo for PCR

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597 CAGCAGATCATCTTCGCTTTATGCGAAGC 628
 Db 17 CAGCAGATCTCTTCCTTTACGACCAATGC 48
 RESULT 7
 US-08-586-676E-11
 Sequence 11, Application US/08586676E
 Patent No. 5972698
 GENERAL INFORMATION:
 APPLICANT: Filtz, Hans,
 APPLICANT: Sommerhoff, Christian
 TITLE OF INVENTION: Tryptase Inhibitor
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 5972698artis Corporation, Patent and Trademark Department
 STREET: 564 Morris Avenue
 CITY: Summit
 STATE: New Jersey
 COUNTRY: US
 ZIP: 07901-1027
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/586,676E
 FILING DATE: 25-JAN-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PC7/EP94/02445
 FILING DATE: 25-JUL-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 93111930.9
 FILING DATE: 26-JUL-1993
 ATTORNEY/AGENT INFORMATION:

```

NAME: Pfeiffer, Hsena J.
REGISTRATION NUMBER: 22,640
REFERENCE/DOCKET NUMBER: 4 20076/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 522 6940
TELEFAX: (908) 522 6955
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: synthetic DNA
US-08-386-676E-11

Query Match      0.8%; Score 20.8; DB 2; Length 48;
Best Local Similarity 78.1%; Pred. No. 2.9e+03;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy      597 CAGCAGATCATCTCTGCTTTAGTGGCAAGC 628
          ||||| ||||| ||||| ||||| ||||| ||
Db      17 CAGCAAGATCTCTCTTCTTTCAGCAGCAATGC 48

RESULT 8.
US-09-641-638-1290/c
Sequence 1290, Application US/09641638
Patent No. 6432648
GENERAL INFORMATION:
APPLICANT: Blumenfeld, Marta
APPLICANT: Bouguetelerc, Lydie
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
TITLE OF INVENTION: GENES INVOLVED IN ARCHIDONIC ACID METABOLISM
FILE REFERENCE: GENST.051CP1
CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
SOFTWARE: Patent.pm
SEQ ID NO 1290
LENGTH: 47
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 10-508-191 : polymorphic base C or T
US-09-641-638-1290

Query Match      0.7%; Score 20.6; DB 4; Length 47;
Best Local Similarity 64.4%; Pred. No. 3.3e+03;
Matches 29; Conservative 1; Mismatches 15; Indels 0; Gaps 0;

Oy      2632 AGCCCATAAAGACCCAGCATCAGTCGAGGAGAGAGAAATCA 2676
          | |||| | |||| | || | | | |||| | || |||| | |
Db      47 AACCCAGAAAAACCTCTCCAGCAGRAAGTAGTGAGAGAAAAACA 3

RESULT 9
US-08-952-793-244
Sequence 244, Application US/08952793
Patent No. 6280932
GENERAL INFORMATION:
APPLICANT: PARMA, et al.

```

```

NAME: Pfeiffer, Hsena J.
REGISTRATION NUMBER: 22,640
REFERENCE/DOCKET NUMBER: 4 20076/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 522 6940
TELEFAX: (908) 522 6955
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: synthetic DNA
US-08-386-676E-11

Query Match      0.8%; Score 20.8; DB 2; Length 48;
Best Local Similarity 78.1%; Pred. No. 2.9e+03;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy      597 CAGCAGATCATCTCTGCTTAGTGGCAAGC 628
          ||||| ||||| ||||| ||||| ||||| ||
Db      17 CAGCAAGATCTCTCTTTCATGACGCAATGC 48

RESULT 8.
US-09-641-638-1290/c
Sequence 1290, Application US/09641638
Patent No. 6432648
GENERAL INFORMATION:
APPLICANT: Blumenfeld, Marta
APPLICANT: Bouguetelerc, Lydie
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
TITLE OF INVENTION: GENES INVOLVED IN ARCHIDONIC ACID METABOLISM
FILE REFERENCE: GENST.051CP1
CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
SOFTWARE: Patent.pm
SEQ ID NO 1290
LENGTH: 47
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 10-508-191 : polymorphic base C or T
US-09-641-638-1290

Query Match      0.7%; Score 20.6; DB 4; Length 47;
Best Local Similarity 64.4%; Pred. No. 3.3e+03;
Matches 29; Conservative 1; Mismatches 15; Indels 0; Gaps 0;

Oy      2632 AGCCATAAAGACCCAGCATCAGTCGAGGAGAGGAATCA 2676
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Db      47 AACCCAGAAAAACCTCTCCACGAGAGTAGTGAGAGAAAAACA 3

RESULT 9
US-08-952-793-244
Sequence 244, Application US/08952793
Patent No. 6280932
GENERAL INFORMATION:
APPLICANT: PARMA, et al.

```

TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
NUMBER OF SEQUENCES: 390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,793
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09455
FILING DATE: 05-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,724
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/472,256
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/472,255
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/477,829
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX40C/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 244:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All C's are 2'-F cytosine
OTHER INFORMATION: All U's are 2'-F uracil
US-08-952-793-244
Query Match 0.7%; Score 20.6; DB 4; Length 52;
Best Local Similarity 65.7%; Pred. No. 3.6e+03;
Matches 23; Conservative 3; Mismatches 9; Indels 0; Gaps 0;
OY 580 CAGAAGATCAGAAACACAGCAGATCCATCTGTC 614
DB 4 CAAGCGGUCAGAAACAACAGCUGGACUACUACGCC 38
RESULT 10
PCT-US96-09455A-244
Sequence 244, Application PC/TUS9609455A
GENERAL INFORMATION:
APPLICANT: PARMA, et al.
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID
NUMBER OF SEQUENCES: 390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.

STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09455A
FILING DATE: 05 JUNE 1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,724
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/472,256
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/477,829
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX40C/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 244:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All C's are 2'-F cytosine
OTHER INFORMATION: All U's are 2'-F uracil
PCT-US96-09455A-244
Query Match 0.7%; Score 20.6; DB 5; Length 52;
Best Local Similarity 65.7%; Pred. No. 3.6e+03;
Matches 23; Conservative 3; Mismatches 9; Indels 0; Gaps 0;
OY 580 CAGAAGATCAGAAACACAGCAGATCCATCTGTC 614
DB 4 CAAGCGGUCAGAAACAACAGCUGGACUACUACGCC 38
RESULT 11
US-08-374-641-40/C
Sequence 40, Application US/08374641
Patent No. 5811231
GENERAL INFORMATION:
APPLICANT: Fatt, Spencer B.
APPLICANT: Todd, Marque D
TITLE OF INVENTION: METHODS AND DIAGNOSTIC KITS FOR
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr. c/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10020
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/374,641
FILING DATE: 12-JUL-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: X-1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
US-08-374-641-40

Query Match 0.7%; Score 20.2; DB 1; Length 50;
Best Local Similarity 68.3%; Pred. No. 4.7e+03;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 2212 TGAGACATCTGCTGTGATTATGATGAGACTGTACTGG 2252
DB 48 TGACAGACTACTGAGTGTACCGTTGAAGAGAGTGAGCTGG 8

RESULT 12
US-08-553-619B-13
Sequence 13, Application US/08553619B
Patent No. 5919705
GENERAL INFORMATION:
APPLICANT: Dehaan, Petrus T.
TITLE OF INVENTION: Virus Resistant Plants
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5919705artis Crop Protection
STREET: 975 California Avenue
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,619B
FILING DATE: December 1, 1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Marcus-wyner, Lynn
REGISTRATION NUMBER: 34,869
REFERENCE/DOCKET NUMBER: 137-1082/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/354-3588
TELEFAX: 415/857-1125
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
HYPOTHETICAL: NO
ORIGINAL SOURCE:

ORGANISM: oligonucleotide
US-08-553-619B-13

Query Match 0.7%; Score 20.2; DB 2; Length 52;
Best Local Similarity 63.3%; Pred. No. 4.8e+03;
Matches 31; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

OY 1437 TATGATGACAGACATGTGGCGTCAGCTTACGTGAATCAACCTCA 1485
DB 1 TTTGATCCAGACGATGTGTGACGATTTTGTATATCAACTCA 49

RESULT 13
US-08-242-035A-2
Sequence 2, Application US/08242035A
Patent No. 5545717
GENERAL INFORMATION:
APPLICANT: Weisbach, Lawrence
TITLE OF INVENTION: PLASMIAR AND PLASMIAR ANTIBODY
TITLE OF INVENTION: COMPOSITIONS AS MALIGNANT CELL MARKERS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: Wordperfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/242,035A
FILING DATE: May 12, 1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/872,645
FILING DATE: April 21, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/116001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 53
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-242-035A-2

Query Match 0.7%; Score 20.2; DB 1; Length 53;
Best Local Similarity 68.3%; Pred. No. 4.9e+03;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 2203 ATACCAAGTGAGACATCTGCTGTGATTAATGATGAGA 2243
DB 10 ATATCAGACTAAGACAGACAGTGTGTGATTAATGCTGAAA 50

RESULT 14
US-08-477-270-21/C
Sequence 21, Application US/08477270
Patent No. 5629158
GENERAL INFORMATION:
APPLICANT: Uhlen, Mathias
TITLE OF INVENTION: SOLID PHASE DIAGNOSIS OF MEDICAL
TITLE OF INVENTION: CONDITIONS

NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,270
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/261,010
FILING DATE:
APPLICATION NUMBER: US 07/781,157
FILING DATE: 07-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16787/153 DFBC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid;
DESCRIPTION: Synthetic DNA oligonucleotide
US-08-477-270-21

Query Match 0.7%; Score 20.2; DB 1; Length 60;
Best Local Similarity 63.3%; Pred. No. 5.3e+03;
Matches 31; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 863 GTTGGGCCAGCTTATCAAGAGCTCAACCTCCTGAGCTCCAGAG 911
DB 52 GTTGAAGACACTTCTCCCGAGTCACAGTCTTGAAGCTGCAGAG 4

RESULT 15
US-08-758-626-23/C
Sequence 23, Application US/08758626
Patent No. 5736334
GENERAL INFORMATION:
APPLICANT: One Spies
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND PROCESS FOR
TITLE OF INVENTION: AMPLIFYING AND DETECTION OF HEPATITIS B VIRAL DNA
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: One Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,626
FILING DATE: 27-NOV-1996

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/422,018
FILING DATE:
APPLICATION NUMBER: 08/090,755
FILING DATE: JULY 13, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Thomas D. Brainard
REGISTRATION NUMBER: 32,459
REFERENCE/DOCKET NUMBER: 5284.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-4884
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 48
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-08-758-626-23

Query Match 0.7%; Score 20; DB 1; Length 48;
Best Local Similarity 72.2%; Pred. No. 5.3e+03;
Matches 26; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 570 AACACTATCCGAGATGATGAGAACACAGCAGGAT 605
DB 45 AAGAACCAACAGAGATGAGCATGACGACGAGAT 10

RESULT 16
PCT-US94-07684-23/C
Sequence 23, Application US/
GENERAL INFORMATION:
APPLICANT: ABBOTT LABORATORIES
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND PROCESS FOR
TITLE OF INVENTION: AMPLIFYING AND DETECTION OF HEPATITIS B VIRAL DNA
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: One Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/090,755
FILING DATE: JULY 13, 1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Thomas D. Brainard
REGISTRATION NUMBER: 32,459
REFERENCE/DOCKET NUMBER: 5284.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-4884
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 48
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
PCT-US94-07684-23

Query Match 0.7%; Score 20; DB 5; Length 48;
Best Local Similarity 72.2%; Pred. No. 5.3e+03;

Best Local Similarity 65.9%; Pred. No. 5.8e+03;
Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 618 ACTGCCAAGCAGATGATTCAGAGGAGAGACTCCAGACT 661
11 11 11111 1 1 1111 1111 111111
Db 10 ACTCGCCCTGAGAGAGAGAGGAGATCAAGATCTCTGACT 53

RESULT 19
US-08-726-807B-21/c

; Sequence 21, Application US/08726807B
; Patent No. 6090618

; GENERAL INFORMATION:

; APPLICANT: Parmacek, Michael S.

; APPLICANT: Solway, Julian

; TITLE OF INVENTION: PROMOTER FOR SMOOTH MUSCLE CELL

; TITLE OF INVENTION: EXPRESSION

; NUMBER OF SEQUENCES: 55

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: Texas

; COUNTRY: USA

; ZIP: 77210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/726.807B

; FILING DATE: 07-OCT-1996

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/004,868

; FILING DATE: 05-OCT-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: McMillian, Nabeeela R.

; REGISTRATION NUMBER: P-43,363

; REFERENCE/DOCKET NUMBER: ARSB:510

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (512) 418-3000

; TELEFAX: (512) 474-7577

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 47 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-08-726-807B-21

Query Match

Best Local Similarity 91.3%; Pred. No. 6.1e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1762 GGGAAAGCCTTTATGTCAGG 1784
111111 11111111 11111

Db 41 GGGAAAAACCTTTATGGGAGG 19

RESULT 20
US-09-258-367-21/c

; Sequence 21, Application US/09258367
; Patent No. 6114311

; GENERAL INFORMATION:

; APPLICANT: Parmacek, Michael S.

; APPLICANT: Solway, Julian

; TITLE OF INVENTION: PROMOTER FOR SMOOTH MUSCLE CELL EXPRESSION

; FILE REFERENCE: ARCD:310

; CURRENT APPLICATION NUMBER: US/09/258.367

; CURRENT FILING DATE: 1999-02-26

; EARLIER APPLICATION NUMBER: 08/726.807

; EARLIER FILING DATE: 1996-10-07

; NUMBER OF SEQ ID NOS: 55

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 21

; LENGTH: 47

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: Primer

; US-09-258-367-21

Query Match

Best Local Similarity 91.3%; Pred. No. 6.1e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1762 GGGAAAGCCTTTATGTCAGG 1784
111111 11111111 11111

Db 41 GGGAAAAACCTTTATGGGAGG 19

RESULT 21
US-09-546-550-21/c

; Sequence 21, Application US/09546550
; Patent No. 6284743

; GENERAL INFORMATION:

; APPLICANT: Parmacek, Michael S.

; APPLICANT: Solway, Julian

; TITLE OF INVENTION: PROMOTER FOR SMOOTH MUSCLE CELL EXPRESSION

; FILE REFERENCE: ARCD:310

; CURRENT APPLICATION NUMBER: US/09/546.550

; CURRENT FILING DATE: 2000-04-10

; PRIOR APPLICATION NUMBER: 09/258.367

; PRIOR FILING DATE: 1999-02-26

; NUMBER OF SEQ ID NOS: 55

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 21

; LENGTH: 47

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: Primer

; US-09-546-550-21

Query Match

Best Local Similarity 91.3%; Pred. No. 6.1e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1762 GGGAAAGCCTTTATGTCAGG 1784
111111 11111111 11111

Db 41 GGGAAAAACCTTTATGGGAGG 19

RESULT 22
US-09-431-414-21/c

; Sequence 21, Application US/09431414
; Patent No. 6291211

; GENERAL INFORMATION:

; APPLICANT: Parmacek, Michael S.

; APPLICANT: Solway, Julian

; TITLE OF INVENTION: PROMOTER FOR SMOOTH MUSCLE CELL EXPRESSION

; FILE REFERENCE: ARCD:335

; CURRENT APPLICATION NUMBER: US/09/431.414

; CURRENT FILING DATE: 1999-11-01

; EARLIER APPLICATION NUMBER: 08/726.807

; NUMBER OF SEQ ID NOS: 55

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 21

; LENGTH: 47

; TYPE: DNA

; ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Primer
US-09-431-414-21

Query Match 0.7%; Score 19.8; DB 4; Length 47;
Best Local Similarity 91.3%; Pred. No. 6.1e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1762 GGGAAAGCCTTTATGTCAGG 1784
||||| ||||||| |||||
DB 41 GGGAAACCTTTATGGCAGG 19

RESULT 23
US-09-225-670-21/c
Sequence 21, Application US/09225670
Patent No. 6297221
GENERAL INFORMATION:
APPLICANT: PARMACER, MICHAEL S.
TITLE OF INVENTION: PROMOTER FOR SMOOTH MUSCLE CELL EXPRESSION
FILE REFERENCE: ARSB:526
CURRENT APPLICATION NUMBER: US/09/225,670
CURRENT FILING DATE: 1999-01-05
EARLIER APPLICATION NUMBER: 08/726,807
EARLIER FILING DATE: 1996-10-07
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
LENGTH: 47
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-225-670-21

Query Match 0.7%; Score 19.8; DB 4; Length 47;
Best Local Similarity 91.3%; Pred. No. 6.1e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1762 GGGAAAGCCTTTATGTCAGG 1784
||||| ||||||| |||||
DB 41 GGGAAACCTTTATGGCAGG 19

RESULT 24
US-09-431-349C-21/c
Sequence 21, Application US/09431349C
Patent No. 6331527
GENERAL INFORMATION:
APPLICANT: PARMACER, MICHAEL S.
APPLICANT: SOLWAY, JULIAN
TITLE OF INVENTION: PROMOTER FOR SMOOTH MUSCLE CELL EXPRESSION
FILE REFERENCE: ARSB:526
CURRENT APPLICATION NUMBER: US/09/431,349C
CURRENT FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: 09/225,670
PRIOR FILING DATE: 1999-01-05
PRIOR APPLICATION NUMBER: 08/726,807
PRIOR FILING DATE: 1996-10-07
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
LENGTH: 47
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-431-349C-21

Query Match 0.7%; Score 19.8; DB 4; Length 47;
Best Local Similarity 91.3%; Pred. No. 6.1e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1762 GGGAAAGCCTTTATGTCAGG 1784
||||| ||||||| |||||
DB 41 GGGAAACCTTTATGGCAGG 19

RESULT 25
US-08-863-813A-47
Sequence 47, Application US/08863813A
Patent No. 6140466
GENERAL INFORMATION:
APPLICANT: Barbas III, Carlos F.
APPLICANT: Gottesfeld, Joel M.
TITLE OF INVENTION: ZINC FINGER PROTEIN DERIVATIVES
TITLE OF INVENTION: AND METHODS THEREFOR
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/863,813A
FILING DATE: 27-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/676,318
FILING DATE: 18-JUL-1996
APPLICATION NUMBER: 08/183,119
FILING DATE: 18-JAN-1996
APPLICATION NUMBER: US95/00829
FILING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A., Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 08401/010001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 57 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-08-863-813A-47

Query Match 0.7%; Score 19.8; DB 3; Length 57;
Best Local Similarity 77.4%; Pred. No. 7e+03;
Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1247 GGGGACACGTGGGGAAGCCTTATGCTTGC 1277
||||| ||||||| ||||||| |||||
DB 3 GGAGGAGACCGGTGAGAGCCTTATGCTTGC 33

RESULT 26
US-09-037-990B-60/c
Sequence 60, Application US/09037990B
Patent No. 6248519
GENERAL INFORMATION:
APPLICANT: ENGEL, Stacia R.

DESCENZO, Richard A.
MORENZONI, Richard A.
IRELAN, Nancy A.
TITLE OF INVENTION: DETECTION OF FERMENTATION-RELATED MICROORGANISMS
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037,990B
FILING DATE: 11-Mar-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Sharp, Jeffrey S.
REGISTRATION NUMBER: 31,879
REFERENCE/DOCKET NUMBER: 29520/30001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-09-037-990B-60

Query Match 0.7%; Score 19.8; DB 4; Length 59;
Best Local Similarity 63.8%; Pred. No. 7.1e+03;
Matches 30; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1194 AAGAAATGTGGCAGAGCTTAGCTGAAGTCAAACTCATTTACCCA 1240
DB 53 AAAAAATGTGTAGACCTTGGCGAGTAAAGCCAGGCTCACCACCCA 7

RESULT 27
US-08-461-184-9/c
Sequence 9, Application US/08461184
Patent No. 5631158
GENERAL INFORMATION:
APPLICANT: DORAI, HAIMANTI
APPLICANT: OPPERMANN, HERMANN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HIGH PROTEIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES, INC
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 07148
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,184
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/143,498
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KELLEY, ROBIN D
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: CRP093
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7100
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 56 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc.feature
LOCATION: 1..56
OTHER INFORMATION: /note="PACISIG"
US-08-461-184-9

Query Match 0.7%; Score 19.6; DB 1; Length 56;
Best Local Similarity 73.5%; Pred. No. 8e+03;
Matches 25; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 567 GGAACACTATCCAGAGATCAGAAACACAGC 600
DB 51 GGAACAGCAATCCAGAACATCAGCACCAACAGC 18

RESULT 28
US-08-463-675-9/c
Sequence 9, Application US/08463675
Patent No. 5658763
GENERAL INFORMATION:
APPLICANT: DORAI, HAIMANTI
APPLICANT: OPPERMANN, HERMANN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HIGH PROTEIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES, INC
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 07148
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,675
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/143,498
FILING DATE: 25-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: KELLEY, ROBIN D
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: CRP093
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7100
TELEFAX: 617/248-7100

;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 56 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: CDNA
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: 1..56
;; OTHER INFORMATION: /note= "PACISIG"
US-08-463-675-9

Query Match 0.7%; Score 19.6; DB 1; Length 56;
Best Local Similarity 73.5%; Pred. No. 8e+03;
Matches 25; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 567 GGAAGACACTATCCAGAGATCAGAACACAGC 600
DB 51 GGAAGCAGGAATCCAGACATCAGCACCACAGC 18

RESULT 29
US-08-464-589-9/C
;; Sequence 9, Application US/08464589
;; Patent No. 5733782
;; GENERAL INFORMATION:
;; APPLICANT: DORAI, HAIMANTI
;; APPLICANT: OPPERMAN, HERMANN
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HIGH PROTEIN
;; TITLE OF INVENTION: PRODUCTION FROM NON-NATIVE DNA
;; NUMBER OF SEQUENCES: 10
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES, INC
;; STREET: 45 SOUTH STREET
;; CITY: HOPKINTON
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 07148
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/464,589
;; FILING DATE: 05-JUN-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/143,498
;; FILING DATE: 25-OCT-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: KELLEY, ROBIN D
;; REGISTRATION NUMBER: 34,637
;; REFERENCE/DOCKET NUMBER: CRP093
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617/248-7000
;; TELEFAX: 617/248-7100
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 56 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: CDNA
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: 1..56
;; OTHER INFORMATION: /note= "PACISIG"
US-08-464-589-9

Query Match 0.7%; Score 19.6; DB 1; Length 56;
Best Local Similarity 73.5%; Pred. No. 8e+03;

Matches 25; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 567 GGAAGACACTATCCAGAGATCAGAACACAGC 600
DB 51 GGAAGCAGGAATCCAGACATCAGCACCACAGC 18

RESULT 30
US-08-406-030A-8
;; Sequence 8, Application US/08406030A
;; Patent No. 6270989
;; GENERAL INFORMATION:
;; APPLICANT: Treco, Douglas A.
;; APPLICANT: Heartlein, Michael W.
;; APPLICANT: Hauge, Brian M.
;; APPLICANT: Selden, Richard F
;; TITLE OF INVENTION: Protein Production and Delivery
;; NUMBER OF SEQUENCES: 30
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
;; STREET: Two Millitia Drive
;; CITY: Lexington
;; STATE: Massachusetts
;; COUNTRY: USA
;; ZIP: 02173
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/406,030A
;; FILING DATE: 17-MAR-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/243,391
;; FILING DATE: 13-MAY-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/985,586
;; FILING DATE: 03-DEC-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/911,533
;; FILING DATE: 10-JUL-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/787,840
;; FILING DATE: 05-NOV-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/789,188
;; FILING DATE: 05-NOV-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US93/11704
;; FILING DATE: 02-DEC-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US92/09627
;; FILING DATE: 05-NOV-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Granahan, Patricia
;; REGISTRATION NUMBER: 32,227
;; REFERENCE/DOCKET NUMBER: TKT95-01
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 861-6240
;; TELEFAX: (617) 861-9540
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 60 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
US-08-406-030A-8

Query Match 0.7%; Score 19.6; DB 4; Length 60;
Best Local Similarity 66.7%; Pred. No. 8.4e+03;

ADDRESSEE: CURTIS, MORRIS & SAFORD, P.C.
STREET: 530 FIFTH AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,210A
FILING DATE: 05-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOMALSKI, THOMAS J.
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 454310-2690
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-840-3333
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-417-210A-99

Query Match
Best Local Similarity 70.3%; Score 19.4; DB 2; Length 43;
Matches 26; Conservative 0; Mismatches 11; Indels 0;

QY 2223 TGTGTGATTCATGACGACTGCTAGCTAGTAACT 2259
1 TTTGTATCGTAATGATGATGACACTGACAGTAAAT 37

RESULT 34
US-09-641-638-760/c
Sequence 760, Application US/09641638
Patent No. 6432648
GENERAL INFORMATION:
APPLICANT: Blumenfeld, Marta
APPLICANT: Bougueleret, Lydie
APPLICANT: Chumakov, Ilya
APPLICANT: Cohen, Annick
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REFERENCE: GENSET.051CPI
CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
SOFTWARE: Patentl.pm
SEQ ID NO 760
LENGTH: 47
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 12-400-217 : polymorphic base A or G
US-09-641-638-760

Query Match
Best Local Similarity 61.7%; Score 19.4; DB 4; Length 47;
Matches 29; Conservative 1; Mismatches 17; Indels 0;

QY 1460 TCACCTTAGCTGGAATCAACCTCAAAACACACACAGGACACT 1506
47 TGACCTTAGTTGAAATAATGACACGATGATTCAGTACAGAACACT 1

RESULT 35
US-08-417-210A-106/c
Sequence 106, Application US/08417210A
Patent No. 5863542
GENERAL INFORMATION:
APPLICANT: PAOLETTI, ENZO
APPLICANT: TARTAGLIA, JAMES
APPLICANT: COX, WILLIAM T.
TITLE OF INVENTION: IMMUNODEFICIENCY RECOMBINANT POXYVIRUS
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: CURTIS, MORRIS & SAFORD, P.C.
STREET: 530 FIFTH AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,210A
FILING DATE: 05-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOMALSKI, THOMAS J.
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 454310-2690
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-840-3333
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
LENGTH: 56 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-417-210A-106

Query Match
Best Local Similarity 70.3%; Score 19.4; DB 2; Length 56;
Matches 26; Conservative 0; Mismatches 11; Indels 0;

QY 2223 TGTGTGATTCATGACGACTGCTAGCTAGTAACT 2259
40 TTTGTATCGTAATGATGATGACACTGACAGTAAAT 4

RESULT 36
US-08-973-965-1/c
Sequence 1, Application US/08973965
Patent No. 6033881
GENERAL INFORMATION:
APPLICANT: HIMMLER, Gottfried
APPLICANT: SCHLEDERER, Thomas
TITLE OF INVENTION: PROCESS FOR THE TRANSCRIPTIONLESS AMPLIFICATION OF
FILE REFERENCE: 030560-055
CURRENT APPLICATION NUMBER: US/08/973,965
CURRENT FILING DATE: 1998-04-06
EARLIER APPLICATION NUMBER: AT A 1007/95
EARLIER FILING DATE: 1995-06-13

EARLIER APPLICATION NUMBER: PCT/AT96/00106
EARLIER FILING DATE: 1996-06-13
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO: 1
LENGTH: 41
TYPE: DNA
ORGANISM: synthetic construct
US-08-973-965-1

Query Match 0.7%; Score 19.2; DB 3; Length 41;
Best Local Similarity 75.0%; Pred. No. 8.7e+03;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Y 1237 CCCACGAGGCGCACACTGGGAGAACCT 1268
DB 34 CCCACGAGGAGCTGCTGTTAGAGGCT 3

RESULT 37

US-08-444-818-229
Sequence 229, Application US/08444818
Patent No. 6150087
GENERAL INFORMATION:
APPLICANT: Chien, David Y.
APPLICANT: Rutter, William J.
TITLE OF INVENTION: NANOV Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,818
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,590
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Harbin, Ailsa A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110,002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)359-3876
TELEFAX: (508)359-3885
INFORMATION FOR SEQ ID NO: 229:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "adaptor in an expression
cassette."
US-08-444-818-229

Query Match 0.7%; Score 19.2; DB 3; Length 44;
Best Local Similarity 67.5%; Pred. No. 9.2e+03;
Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Y 331 TGGAAATTCATCTTAAACCAAACTCATGTCTAGCT 370
DB 5 TGGAAATTCATATGAGACCTTAAGTATTACTAGCT 44

RESULT 38

US-08-171-389-100
Sequence 100, Application US/08171389
Patent No. 5578444
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-directed DNA Binding
Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 641
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,389
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0175/G19P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0960
TELEFAX: (415) 324-0880
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human CYP2C8 gene for cytochrome
P-450
US-08-171-389-100

Query Match 0.7%; Score 19.2; DB 1; Length 45;
Best Local Similarity 75.0%; Pred. No. 9.3e+03;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Y 1353 TACATTTGACGAGAGCTGAGCAGGCTTAG 1384
DB 3 TAAATTAGCAGGAGGTGTTAATAAACTTGG 34

RESULT 39
US-08-123-936-100

Sequence 100, Application US/08123936
Patent No. 5726014
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
TITLE OF INVENTION: Screening Assay for the Detection of
NUMBER OF SEQUENCES: 640
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,936
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0075.32/G19P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human CYP2C8 gene for cytochrome
INDIVIDUAL ISOLATE: P-450
US-08-123-936-100
Query Match 0.7%; Score 19.2; DB 1; Length 45;
Best Local Similarity 75.0%; Pred. No. 9.3e+03;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
OY 1353 TACATTGCAGGAGTGTGACCAAGCTTTAG 1384
DB 3 TAAATTACAGGAGTGTATATAAATTGG 34
RESULT 40
US-08-475-228A-100
Sequence 100, Application US/08475228A
Patent No. 5869241
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods

NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,228A
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 4600-0175.21/G19P3D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human CYP2C8 gene for cytochrome
INDIVIDUAL ISOLATE: P-450
US-08-475-228A-100
Query Match 0.7%; Score 19.2; DB 2; Length 45;
Best Local Similarity 75.0%; Pred. No. 9.3e+03;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
OY 1353 TACATTGCAGGAGTGTGACCAAGCTTTAG 1384
DB 3 TAAATTACAGGAGTGTATATAAATTGG 34
RESULT 41
US-08-482-080A-100
Sequence 100, Application US/08482080A
Patent No. 6010849
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive

CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,080A
FILING DATE: 07-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/171,389
FILING DATE: 20-DEC-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Brady, John F.
REGISTRATION NUMBER: 39,118
REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0880
TELEFAX: (650) 324-0960
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human CYP2C8 gene for cytochrome
INDIVIDUAL ISOLATE: P-450
US-08-482-080A-100

Query Match 0.7%; Score 19.2; DB 3; Length 45;
Best Local Similarity 75.0%; Pred. No. 9.3e+03;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1353 TACATTTCAGGAGCTGTGACCAAGCCTTAG 1384
|| ||| ||||| ||||| || |||||
Db 3 TAAATTAGCAGGAGTGTATATAAAACTTTGG 34

RESULT 42
US-09-354-947-100
Sequence 100, Application US/09354947
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City

STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/354,947
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/482,080
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/171,389
FILING DATE: 20-DEC-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Brady, John F.
REGISTRATION NUMBER: 39,118
REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0880
TELEFAX: (650) 324-0960
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human CYP2C8 gene for cytochrome
INDIVIDUAL ISOLATE: P-450
US-09-354-947-100

Query Match 0.7%; Score 19.2; DB 4; Length 45;
Best Local Similarity 75.0%; Pred. No. 9.3e+03;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1353 TACATTTCAGGAGCTGTGACCAAGCCTTAG 1384
|| ||| ||||| ||||| || |||||
Db 3 TAAATTAGCAGGAGTGTATATAAAACTTTGG 34

RESULT 43
PCT-US93-12388-100
Sequence 100, Application PC/TUS9312388
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Sequence-Directed DNA Binding
Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 641
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:

RESULT 44
 US-08-859-649-10
 Sequence 10, Application US/08859649
 Patent No. 5874060
 GENERAL INFORMATION:
 APPLICANT: Armour, Kathryn L.
 APPLICANT: Carr, Francis J.
 APPLICANT: Old, Lloyd J.
 APPLICANT: Klamura, Kunio
 APPLICANT: Garin-Chesa, Pilar
 TITLE OF INVENTION: Recombinant Human Anti-Lewis Y
 TITLE OF INVENTION: Antibodies
 NUMBER OF SEQUENCES: 33
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 2730 Sand Hill Road
 CITY: Menlo Park
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 94025
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/859,649
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:

RESULT 45
US-08-207-861-10
Sequence 10, Application US/08207861
Patent No. 6310185

GENERAL INFORMATION:

APPLICANT: Amour, Kathryn L.
APPLICANT: Carr, Francis J.
APPLICANT: Old, Lloyd J.
APPLICANT: Kitamura, Kunio
APPLICANT: Garin-Chesa, Pilar

TITLE OF INVENTION: Recombinant Human Anti-Lewis Y
TITLE OF INVENTION: Antibodies

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 2730 Sand Hill Road
CITY: Menlo Park
STATE: California
COUNTRY: U.S.A.

ZIP: 94025

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/207,861
FILING DATE: 08-MAR-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7606-027

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown

MOLECULE TYPE: DNA
US-08-207-861-10

Query Match 0.7%; Score 19.2; DB 4; Length 48;
Best Local Similarity 67.5%; Pred. No. 9.7e+03;
Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Oy 472 TTTTCTCCAGTCAGAGCTTCACCCACATGTGTGCT 511
Db 1 TTGGCCCGAGTAAGCAACACGACGACCATCAGGGTGCT 40

RESULT 46

US-08-431-527A-6
Sequence 6, Application US/08431527A
Patent No. 5843650
GENERAL INFORMATION:
APPLICANT: David Segev
TITLE OF INVENTION: No. 5843650-enzymatic method for detecting nucleic acid sequer
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark M. Friedman c/o Robert Shelnbein
STREET: 2940 Birchtree space lane
CITY: Silver Spring
STATE: Maryland
COUNTRY: United States of America
ZIP: 20906
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
COMPUTER: Twinhead Slimnote-890TX
OPERATING SYSTEM: MS DOS version 6.2,
SOFTWARE: Word for Windows version 3.11
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431.527A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REFERENCE/DOCKET NUMBER: 128/8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972-3-6938541
TELEFAX: 972-3-6938542
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 58
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-431-527A-6

Query Match 0.7%; Score 19.2; DB 2; Length 58;
Best Local Similarity 62.5%; Pred. No. 1.1e+04;
Matches 30; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Oy 73 TACCTGATTCGGCTTCAGATCGGCGCTGCACCCGCGTTCATC 120
Db 1 TACATGTGTACAGTTCCTCGATGGCGGCGATGAACCGAGGCCCATC 48

RESULT 47

US-08-485-355B-53
Sequence 53, Application US/08485355B
Patent No. 6177075
GENERAL INFORMATION:
APPLICANT: Christian, P. D., Gordon, K. H.J., Hanzlik, T. N.
TITLE OF INVENTION: Insect Viruses and Their Uses in
Protecting Plants
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr, Hohbach Test Albritton & Herbert LLP
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,355B
FILING DATE: 07-Jun-1995
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/440,522
FILING DATE: 12-MAY-1995
APPLICATION NUMBER: US 08/089,372
FILING DATE: 08-JUL-1993
APPLICATION NUMBER: AU PL4081/92
FILING DATE: 14-AUG-1992

ATTORNEY/AGENT INFORMATION:

NAME: Trecaulin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-58631-2/RFT/DSS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299

INFORMATION FOR SEQ ID NO: 53:

SEQUENCE CHARACTERISTICS:
LENGTH: 59 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: DNA
MOLECULE TYPE: unknown
SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-08-485-355B-53

Query Match 0.7%; Score 19.2; DB 4; Length 59;
Best Local Similarity 62.5%; Pred. No. 1.1e+04;
Matches 30; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Oy 759 GTGATATAGGGTCCAGCCCTGAACGGAGGCGCATCTAGAGGAACA 806
Db 1 GGGATCCACAGTTCCTGCTCCCGGAGCGTAATATAGGGGAACA 48

RESULT 48

US-08-373-124A-185/C
Sequence 185, Application US/08373124A
Patent No. 5646042
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwigen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage

COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Wardburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 185:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-373-124A-185

Query Match 0.7%; Score 19; DB 1; Length 38;
Best Local Similarity 71.4%; Pred. No. 9.6e+03;
Matches 25: Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 35 CTCCTCTTAAGTCTTCCACACCTGCTCT 69
DB 38 CTCCTCTTTCGGCTTCGGCCTCATCAGCTCT 4

RESULT 49
US-08-435-628-185/c
Sequence 185, Application US/08435628
Patent No. 5817796
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwigen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
SUITE: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,628
FILING DATE: 05-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/373,124

FILING DATE: January 13, 1995
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Wardburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 185:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-435-628-185

Query Match 0.7%; Score 19; DB 1; Length 38;
Best Local Similarity 71.4%; Pred. No. 9.6e+03;
Matches 25: Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 35 CTCCTCTTAAGTCTTCCACACCTGCTCT 69
DB 38 CTCCTCTTTCGGCTTCGGCCTCATCAGCTCT 4

RESULT 50
US-09-609-816-13
Sequence 13, Application US/09609816
Patent No. 6436684
GENERAL INFORMATION:
APPLICANT: Woodage, Trevor
APPLICANT: Wei, Minh Hui
APPLICANT: Kodira, Chinappa
APPLICANT: Beasley, Ellen
APPLICANT: DiFrancesco, Valentina
TITLE OF INVENTION: ISOLATED HUMAN DRUG-METABOLIZING
PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
TITLE OF INVENTION: DRUG-METABOLIZING PROTEINS, AND USES THEREOF
FILE REFERENCE: CLO00669PCT
CURRENT APPLICATION NUMBER: US/09/609,816
CURRENT FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/192,408
PRIOR FILING DATE: 2000-03-27
PRIOR APPLICATION NUMBER: 60/212,725
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: 09/609,816
PRIOR FILING DATE: 2000-07-03
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 13
TYPE: DNA
LENGTH: 46
ORGANISM: HUMAN
US-09-609-816-13

Query Match 0.7%; Score 19; DB 4; Length 46;
Best Local Similarity 62.2%; Pred. No. 1.1e+04;
Matches 28: Conservative 1; Mismatches 16; Indels 0; Gaps 0;

QY 2708 CATCCCTCTTCACGACGCTGTTTGGTCAATAAATCT 2752
DB 2 CAACCCCTCTTCGCTTAACCTCTATCTCTCTAAACACATCT 46

Fri Jun 6 11:21:42 2003

us-09-898-556a-3.szlm60.mri

Page 24

Search completed: June 4, 2003, 10:26:12
Job time : 167 secs

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OM nucleic - nucleic search, using sw model

Run on: June 4, 2003, 06:49:48 ; Search time 3825 Seconds
(without alignments)
11736.965 Million cell updates/sec

Title: US-09-898-556A-3

Perfect score: 2772

Sequence: 1 cagcgcgcttaagctggtg.....ttctaccatccaccct 2772

Scoring table:

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 146654

Minimum DB seq length: 0

Maximum DB seq length: 60

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estcpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	34	1.2	58	AA757305	AA757305 ab96e09.s
C 2	34	1.2	60	AA834171	AA834171 cflaell.s
C 3	28.4	1.0	58	AA864103	AA864103 vna2502.r
C 4	28.2	1.0	52	AA425976	AA425976 zw1b06.f
C 5	27.6	1.0	58	AA994682	AA994682 cou58c08.s
C 6	26.6	1.0	58	AA1597270	AA1597270 v154d09.x

7	26.4	1.0	46	AA902889	AA902889 cj49g04.s
C 8	25.8	0.9	55	AA136306	AA136306 zn89ec02.s
C 9	24.6	0.9	45	AA513479	AA513479 1m0359p21
C 10	24.4	0.9	50	AA948106	AA948106 on51a04.s
C 11	23.8	0.9	38	R37288	R37288 yf67a06.s1
C 12	23.8	0.9	59	B1650525	B1650525 6032969501
C 13	23.6	0.9	46	AA867748	AA867748 vx16a12.r
C 14	23.4	0.8	49	AA227017	AA227017 zrl9c09.r
C 15	23.4	0.8	60	BF638864	BF638864 NF060102P
C 16	22.8	0.8	37	TA83009	TA83009 yd39a12.r1
C 17	22.8	0.8	34	AA352619	AA352619 1M0091111
C 18	22.8	0.8	55	A1687537	A1687537 lp88f10.x
C 19	22.8	0.8	56	CNS020B3	AL175368 Tetraodon
C 20	22.6	0.8	55	B1963825	B1963825 i6e5a07.x
C 21	22.6	0.8	58	AA767515	AA767515 oad4a03.s
C 22	22.6	0.8	60	AL757225	AL757225 Arabidops
C 23	22.2	0.8	43	AA227334	AA227334 zrl7b11.r
C 24	22.2	0.8	52	BMS66527	BMS66527 Kj63e09.y
C 25	22	0.8	48	A2310125	A2310125 1M0018M20
C 26	22	0.8	55	A2665324	A2665324 1M0546007
C 27	22	0.8	58	A1051772	A1051772 ox45e08.s
C 28	22	0.8	59	AA442276	AA442276 1M0234P19
C 29	21.8	0.8	34	A1722821	A1722821 fc32a11.y
C 30	21.6	0.8	58	AA139470	AA139470 mr82e10.r
C 31	21.4	0.8	56	R67248	R67248 y131g11.r1
C 32	21.2	0.8	43	AA059057	AA059057 zf63b10.s
C 33	21.2	0.8	49	R75644	R75644 y159f01.s1
C 34	21.2	0.8	50	AU105724	AU105724 AU105724
C 35	21.2	0.8	51	B02962	B02962 CSR1-164B7-
C 36	21.2	0.8	52	BM692135	BM692135 NF048A11S
C 37	21	0.8	40	A2595836	A2595836 1M0408008
C 38	21	0.8	42	AU256802	AU256802 AU256802
C 39	21	0.8	50	AU103658	AU103658 AU103658
C 40	21	0.8	50	AU105956	AU105956 AU105956
C 41	21	0.8	58	AA976008	AA976008 cq29b04.s
C 42	20.8	0.8	49	AA957851	AA957851 AV957851
C 43	20.8	0.8	56	A2666147	A2666147 1M0548C04
C 44	20.8	0.8	60	A2566268	A2566268 219PVD10
C 45	20.6	0.7	52	BG575662	BG575662 602598728
C 46	20.6	0.7	52	TA8328D010	TA8328D010 T. brucei
C 47	20.6	0.7	55	AA494740	AA494740 fail1h10.r
C 48	20.6	0.7	55	BH862808	BH862808 SALK_0906
C 49	20.6	0.7	58	A1955368	A1955368 w12e02.x
C 50	20.4	0.7	50	A2766605	A2766605 1M0564L13
C 51	20.4	0.7	52	CNS046B5	AL276458 Tetraodon
C 52	20.4	0.7	48	AA744527	AA744527 ny79e02.s
C 53	20.2	0.7	53	AA947644	AA947644 cq32a05.s
C 54	20.2	0.7	47	BH790449	BH790449 SALK_0570
C 55	20.2	0.7	50	AU104726	AU104726 AU104726
C 56	20.2	0.7	52	AA004892	AA004892 zb87g03.r
C 57	20.2	0.7	55	B1909391	B1909391 603065494
C 58	20.2	0.7	58	A2615585	A2615585 1M0445G07
C 59	20.2	0.7	60	AQ026349	AQ026349 I(3)ne054
C 60	20	0.7	45	AA463271	AA463271 zx97h11.s
C 61	20	0.7	48	A2596241	A2596241 1M0409F23
C 62	20	0.7	50	AU105723	AU105723 AU105723
C 63	20	0.7	53	AQ050186	AQ050186 nbxb0003c
C 64	20	0.7	54	CNS02XT9	AL218790 Tetraodon
C 65	20	0.7	55	A1491955	A1491955 f007a11.x
C 66	20	0.7	56	A2490288	A2490288 1M0323J09
C 67	20	0.7	57	AU260330	AU260330 AU260330
C 68	20	0.7	58	HA9949	HA9949 y025g03.r1
C 69	20	0.7	58	AA025909	AA025909 I(2)K0950
C 70	20	0.7	58	A2796876	A2796876 2M0052K18
C 71	19.8	0.7	40	W85183	W85183 mF50d11.r1
C 72	19.8	0.7	43	A277560	A277560 2M0012102
C 73	19.8	0.7	47	A2778132	A2778132 2M0013N08
C 74	19.8	0.7	50	AU102264	AU102264 AU102264
C 75	19.8	0.7	50	AU102267	AU102267 AU102267
C 76	19.8	0.7	54	NS9739	NS9739 yv56f04.r1
C 77	19.8	0.7	55	B1143779	B1143779 602907244
C 78	19.8	0.7	58	AA637409	AA637409 vU06c01.r
C 79	19.8	0.7	58	H55542	H55542 CHR220481.C

80	19.8	0.7	58	17	BH412160	BH412160 1007025t1	153	18.8	0.7	52	17	A2458224	A2458224 1M0262C07
81	19.8	0.7	60	9	AA762539	AA762539 vW06e11.r	154	18.8	0.7	52	17	BH897343	BH897343 3526.1.7-
82	19.6	0.7	37	10	AV966495	AV966495 AV966495	155	18.8	0.7	55	9	AA034529	AA034529 m151b12.r
83	19.6	0.7	37	17	AZ66528	AZ66528 1M0548A18	156	18.8	0.7	55	9	A2627999	A2627999 1M0476G10
84	19.6	0.7	44	17	AZ862805	AZ862805 2M0170H11	157	18.8	0.7	56	14	H57036	H57036 yf09d01.t1
85	19.6	0.7	49	14	H03417	H03417 yf48f06.s1	158	18.8	0.7	56	17	AZ783539	AZ783539 2M0025G21
86	19.6	0.7	50	9	AU105715	AU105715 AU105715	159	18.8	0.7	56	17	AZ809245	AZ809245 2M007310H
87	19.6	0.7	50	9	AU105717	AU105717 AU105717	160	18.8	0.7	56	17	AZ822908	AZ822908 2M0096M05
88	19.6	0.7	50	9	AU105721	AU105721 AU105721	161	18.8	0.7	56	17	BH614932	BH614932 KC00927-5
89	19.6	0.7	50	9	AU106031	AU106031 AU106031	162	18.8	0.7	57	17	DR16K1T	DR16K1T Dantio Ter
90	19.6	0.7	50	13	BI175138	BI175138 OSTR010p1	163	18.8	0.7	58	17	AG020453	AG020453 Homo sapi
91	19.6	0.7	55	9	AI090302	AI090302 oY81a09..s	164	18.8	0.7	59	17	AL751510	AL751510 Arabidops
92	19.6	0.7	55	14	AI220035	AI220035 G978b07.r	165	18.8	0.7	59	17	TA37F04Q	TA37F04Q T. brucei
93	19.6	0.7	55	14	BO274332	BO274332 Kc50b07.y	166	18.8	0.7	60	10	AM119912	AM119912 sd54e02.y
94	19.6	0.7	55	17	BH895217	BH895217 3526-1..33	167	18.8	0.7	60	17	AZ693621	AZ693621 AST-1HB1
95	19.4	0.7	43	17	AZ641546	AZ641546 1M0504F11	168	18.6	0.7	35	17	BH746336	BH746336 SALK_0373
96	19.4	0.7	48	17	TA1758A01P	TA1758A01P	169	18.6	0.7	41	14	D11997	D11997 HDM0513A04
97	19.4	0.7	50	9	AU102269	AU102269 AU102269	170	18.6	0.7	49	17	AZ455726	AZ455726 1M0258A15
98	19.4	0.7	50	9	AU107324	AU107324 AU107324	171	18.6	0.7	49	17	AZ987326	AZ987326 2M0269B23
99	19.4	0.7	56	9	AA681906	AA681906 vU75f02..r	172	18.6	0.7	50	9	AU104139	AU104139 AU104139
100	19.4	0.7	56	9	AA681906	AA681906 vU75f02..r	173	18.6	0.7	50	9	AU104723	AU104723 AU104723
101	19.4	0.7	57	10	AMS51185	AMS51185 L0074H11-	174	18.6	0.7	50	9	AU104844	AU104844 AU104844
102	19.4	0.7	57	17	AZ812571	AZ812571 2M0079014	175	18.6	0.7	50	9	AU106286	AU106286 AU106286
103	19.4	0.7	57	17	B01045	B01045 CSRL-123g3-	176	18.6	0.7	50	9	AU107205	AU107205 AU107205
104	19.4	0.7	58	9	AA878836	AA878836 OF87F03.s	177	18.6	0.7	50	9	BH865870	BH865870 SALK_1000
105	19.4	0.7	60	13	BM360861	BM360861 8 CDNA_SU	178	18.6	0.7	51	9	AI252090	AI252090 GVS8C05.x
106	19.2	0.7	38	17	AZ797817	AZ797817 2M0054E18	179	18.6	0.7	51	9	AA616601	AA616601 vW66f08.r
107	19.2	0.7	43	9	AA620538	AA620538 ae61b06..s	180	18.6	0.7	52	12	BF635028	BF635028 NF078F12D
108	19.2	0.7	51	17	AZ330155	AZ330155 1M0055E13	181	18.6	0.7	52	12	BF651170	BF651170 NF102E01E
109	19.2	0.7	51	17	AZ852643	AZ852643 2M0155O11	182	18.6	0.7	53	17	AL760278	AL760278 Arabidops
110	19.2	0.7	52	10	AI251382	AI251382 GVS8A02.x	183	18.6	0.7	54	17	AZ841633	AZ841633 2M0139C16
111	19.2	0.7	52	10	BE248989	BE248989 NF030F03D	184	18.6	0.7	55	12	BE881831	BE881831 601504955
112	19.2	0.7	53	17	B0247805	B0247805 TAE25042C	185	18.6	0.7	55	12	AZ849766	AZ849766 2M0151P13
113	19.2	0.7	53	17	B00687	B00687 CSRL-118e7.r	186	18.6	0.7	56	17	AZ328238	AZ328238 1M0051124
114	19.2	0.7	54	17	TA358C03P	TA358C03P	187	18.6	0.7	57	10	TA86H06P	TA86H06P T. brucei
115	19.2	0.7	55	17	BH851672	BH851672 SALK_0733	188	18.6	0.7	57	17	AM873288	AM873288 hm28g07.x
116	19.2	0.7	57	14	BU033638	BU033638 CHR90087.ch	189	18.6	0.7	57	14	H40045	H40045 TAE05038G
117	19.2	0.7	59	13	BU033638	BU033638	190	18.6	0.7	57	14	BH791320	BH791320 SALK_0597
118	19.2	0.7	59	17	AQ026007	AQ026007 EP(2)0456	191	18.6	0.7	58	9	AA411417	AA411417 Gc95h09.x
119	19.2	0.7	59	17	AZ595063	AZ595063 1M0407L21	192	18.6	0.7	58	14	W84003	W84003 m124d09..r1
120	19.2	0.7	59	17	CNS01XVD	AL172210 Telracon	193	18.6	0.7	59	14	B1246259	B1246259 602958824
121	19.2	0.7	60	17	AL763043	AL763043 Arabidops	194	18.6	0.7	59	17	AZ467302	AZ467302 1M0278C02
122	19.2	0.7	40	14	R96580	R96580 YG54B10..r1	195	18.6	0.7	60	9	AL588055	AL588055 AL588055
123	19.2	0.7	43	9	AI014286	AI014286 am46a02.s	196	18.6	0.7	35	17	AZ589053	AZ589053 2M0274C03
124	19.2	0.7	46	17	AZ474604	AZ474604 1M0294G04	197	18.6	0.7	37	9	AI020105	AI020105 ub14f04..r
125	19.2	0.7	47	17	AZ634774	AZ634774 1M0490F16	198	18.6	0.7	40	9	AA972469	AA972469 op42a04..s
126	19.2	0.7	49	9	AI652389	AI652389 zb36b08.s	199	18.6	0.7	40	9	AT766973	AT766973 qx1f03.x
127	19.2	0.7	49	9	AA496619	AA496619	200	18.6	0.7	46	9	AI249431	AI249431 qx02e01.x
128	19.2	0.7	49	14	T56757	T56757 ya71d06..r1	201	18.4	0.7	46	9	AZ633067	AZ633067 1M0488N01
129	19.2	0.7	50	9	BH759224	BH759224 KG00450-3	202	18.4	0.7	47	10	AZ778978	AZ778978 AV834400
130	19.2	0.7	51	14	C00457	C00457 H0MS000696	203	18.4	0.7	48	17	BH614887	BH614887 2M0014AP09
131	19.2	0.7	52	12	BF650846	BF650846 NF097B02E	204	18.4	0.7	48	17	AZ633067	AZ633067 KC02855-3
132	19.2	0.7	53	13	BM566810	BM566810 k106c09.y	205	18.4	0.7	49	17	BE912649	BE912649 601663692
133	19.2	0.7	53	14	BO636166	BO636166 hd05d04.y	206	18.4	0.7	50	12	AZ351330	AZ351330 1M0089013
134	19.2	0.7	53	14	N40810	N40810 yw62g06..r1	207	18.4	0.7	52	14	BF725201	BF725201 v182g06..r
135	19.2	0.7	55	17	AZ566013	AZ566013 215PVC03	208	18.4	0.7	52	14	BF725201	BF725201 bx13c05.y
136	19.2	0.7	55	17	AZ683619	AZ683619 AST-1H8G3	209	18.4	0.7	52	17	CNS02JCZ	CNS02JCZ Tetracodon
137	19.2	0.7	58	9	AI528716	AI528716 m126h06..x	210	18.4	0.7	53	17	AA142590	AA142590 ms10b01.r
138	19.2	0.7	58	13	BG938970	BG938970 cm29f03.y	211	18.4	0.7	55	9	AI481901	AI481901 v181b12.x
139	19.2	0.7	58	13	BI305183	BI305183 ma96c06..r1	212	18.4	0.7	55	9	AA265233	AA265233 m248g05.r
140	19.2	0.7	59	13	BM265911	BM265911 tW37c03.y	213	18.4	0.7	55	9	AA586631	AA586631 m35h07.s
141	19.2	0.7	60	13	BM265911	BM265911 tW37c03.y	214	18.4	0.7	55	9	AA586631	AA586631 m35h07.s
142	19.2	0.7	60	13	BM265911	BM265911 tW37c03.y	215	18.4	0.7	55	9	AA586631	AA586631 m35h07.s
143	19.2	0.7	60	13	BM265911	BM265911 tW37c03.y	216	18.4	0.7	55	9	AA586631	AA586631 m35h07.s
144	18.8	0.7	40	9	AI747109	AI747109 u109f07.x	217	18.4	0.7	55	9	AA586631	AA586631 m35h07.s
145	18.8	0.7	41	17	AA579190	AA579190 nF32b03.s	218	18.4	0.7	55	9	AA586631	AA586631 m35h07.s
146	18.8	0.7	46	9	AA890005	AA890005 aj89h03.s	219	18.4	0.7	55	9	AA586631	AA586631 m35h07.s
147	18.8	0.7	48	17	AZ504252	AZ504252 1M0344F19	220	18.4	0.7	55	9	AA586631	AA586631 m35h07.s
148	18.8	0.7	50	9	AU106934	AU106934 AU106934	221	18.4	0.7	55	9	AA586631	AA586631 m35h07.s
149	18.8	0.7	51	17	B04190	B04190 CSRL-28b9-u	222	18.4	0.7	55	9	AA586631	AA586631 m35h07.s
150	18.8	0.7	52	9	AA659205	AA659205 n192a07.s	223	18.4	0.7	55	9	AA586631	AA586631 m35h07.s
151	18.8	0.7	52	10	AM691164	AM691164 NF038E01S	224	18.4	0.7	55	9	AA586631	AA586631 m35h07.s
152	18.8	0.7	52	10	AM691164	AM691164 NF038E01S	225	18.4	0.7	55	9	AA586631	AA586631 m35h07.s

C 226	18.4	0.7	56	12	BF969804	602272253	C 299	18	0.6	50	9	AA779496
C 227	18.4	0.7	56	17	BH851537	SALK_0731	C 300	18	0.6	50	9	AU102648
C 228	18.4	0.7	56	17	BH855840	SALK_0844	C 301	18	0.6	50	9	AU103059
C 229	18.4	0.7	56	17	BH855841	SALK_0844	C 302	18	0.6	50	9	AU105712
C 230	18.4	0.7	56	17	CNS04G1B		C 303	18	0.6	50	9	AU106906
C 231	18.4	0.7	57	17	BH814102	Tetraodon	C 304	18	0.6	50	9	AA589316
C 232	18.4	0.7	58	14	R52127		C 305	18	0.6	50	17	AZ627991
C 233	18.4	0.7	59	14	AT884443	wm32e08.x	C 306	18	0.6	50	17	BH850602
C 234	18.4	0.7	59	14	T78479	T78479 md68605.s1	C 307	18	0.6	51	13	BM431597
C 235	18.4	0.7	59	14	W64248	W64248 yd95d12.r1	C 308	18	0.6	51	17	AZ491576
C 236	18.4	0.7	59	17	B03913	CSRL-19g10-	C 309	18	0.6	51	17	AZ491576
C 237	18.4	0.7	60	9	AL789128	AL789128 AL789128	C 310	18	0.6	52	9	AA019193
C 238	18.2	0.7	37	9	AL427510	AL427510 m163f10.x	C 311	18	0.6	52	12	BG271387
C 239	18.2	0.7	38	17	AZ9922097	AZ9922097 2M0276D07	C 312	18	0.6	52	12	BG235492
C 240	18.2	0.7	40	9	AT962543	AT962543 wg53g05.x	C 313	18	0.6	53	17	AZ658951
C 241	18.2	0.7	42	14	H71950	H71950 yf98a05.r1	C 314	18	0.6	54	13	B1714368
C 242	18.2	0.7	45	17	AZ437643	AZ437643 1M0226K11	C 315	18	0.6	54	13	B1714368
C 243	18.2	0.7	46	17	AZ828414	AZ828414 2M0105E23	C 316	18	0.6	55	9	AU013239
C 244	18.2	0.7	47	9	AL662579	AL662579 AL662579	C 317	18	0.6	55	12	BF647754
C 245	18.2	0.7	47	17	AZ658529	AZ658529 1M0535C15	C 318	18	0.6	55	12	BG235492
C 246	18.2	0.7	48	13	B1053320	B1053320 BJ053320	C 319	18	0.6	55	13	BJ041372
C 247	18.2	0.7	49	9	AT654317	AT654317 tq90c04.x	C 320	18	0.6	55	17	AZ652948
C 248	18.2	0.7	49	14	BQ089240	BQ089240 K023f10.y	C 321	18	0.6	55	17	DR7LIS
C 249	18.2	0.7	50	9	AU102268	AU102268 AU102268	C 322	18	0.6	55	17	TA312B1Q
C 250	18.2	0.7	50	9	AU103101	AU103101 AU103101	C 323	18	0.6	56	9	AU268876
C 251	18.2	0.7	50	9	AU106666	AU106666 AU106666	C 324	18	0.6	56	10	AM247621
C 252	18.2	0.7	50	9	AU107454	AU107454 AU107454	C 325	18	0.6	56	12	BF120139
C 253	18.2	0.7	51	17	AZ313593	AZ313593 1M0303B05	C 326	18	0.6	56	14	F35060
C 254	18.2	0.7	51	17	CNS02VIL	AL215814 Tetraodon	C 327	18	0.6	56	17	AZ682794
C 255	18.2	0.7	52	9	AA869327	AA869327 vq50f08.r	C 328	18	0.6	56	17	HSMC09F1
C 256	18.2	0.7	52	9	AA888536	AA888536 nw81a04.s	C 329	18	0.6	57	9	A1930814
C 257	18.2	0.7	52	9	A1154969	A1154969 ud82b10.r	C 330	18	0.6	57	13	B1714149
C 258	18.2	0.7	52	9	A1970313	A1970313 wr9e04.x	C 331	18	0.6	57	17	TA348B10P
C 259	18.2	0.7	52	9	AA511416	AA511416 v127e10.r	C 332	18	0.6	58	9	AT719637
C 260	18.2	0.7	52	10	BE042312	BE042312 hk35d07.y	C 333	18	0.6	58	9	AA489706
C 261	18.2	0.7	52	17	AZ337199	AZ337199 1M0067J09	C 334	18	0.6	58	13	BJ077758
C 262	18.2	0.7	52	17	AZ447457	AZ447457 1M0244E08	C 335	18	0.6	58	13	BM434781
C 263	18.2	0.7	53	17	AZ484807	AZ484807 1M031J02	C 336	18	0.6	58	17	AZ320565
C 264	18.2	0.7	53	17	CNS01SD9	AL165078 Tetraodon	C 337	18	0.6	58	17	AZ789611
C 265	18.2	0.7	54	10	AM590712	AM590712 h448a02.x	C 338	18	0.6	58	17	CNS0220S
C 266	18.2	0.7	54	10	AZ944165	AZ944165 2M0205B08	C 339	18	0.6	59	9	AA734809
C 267	18.2	0.7	54	17	BH803546	BH803546 1008104G1	C 340	18	0.6	59	9	AU255513
C 268	18.2	0.7	55	14	A1090915	A1090915 q44e12.s	C 341	18	0.6	59	13	BM128193
C 269	18.2	0.7	55	14	R93606	R93606 yq38c12.s1	C 342	18	0.6	59	17	AZ747439
C 270	18.2	0.7	55	17	AZ788077	AZ788077 2M034M23	C 343	18	0.6	59	17	BH790579
C 271	18.2	0.7	55	17	AZ983943	AZ983943 2M0256G18	C 344	18	0.6	60	9	AA133428
C 272	18.2	0.7	56	17	B00869	B00869 CSRL-121D9-	C 345	18	0.6	60	10	AM548396
C 273	18.2	0.7	56	17	BH214651	BH214651 KC03603-5	C 346	18	0.6	60	10	BE136677
C 274	18.2	0.7	56	17	TA107E04P	AL458969 T. brucei	C 347	18	0.6	60	10	BE136701
C 275	18.2	0.7	57	9	AU259781	AU259781 AU259781	C 348	18	0.6	60	10	BE324712
C 276	18.2	0.7	57	17	AZ465223	AZ465223 1M0275E05	C 349	18	0.6	60	12	BF638499
C 277	18.2	0.7	57	17	AZ803892	AZ803892 2M0064F05	C 350	18	0.6	60	12	BE887234
C 278	18.2	0.7	58	9	AU254156	AU254156 AU254156	C 351	18	0.6	60	13	B1225676
C 279	18.2	0.7	58	17	AZ446605	AZ446605 1M0243A09	C 352	18	0.6	60	13	BJ053947
C 280	18.2	0.7	58	17	AZ772394	AZ772394 1M0583D16	C 353	18	0.6	60	14	H55533
C 281	18.2	0.7	58	17	AZ834846	AZ834846 2M0117F18	C 354	18	0.6	60	17	AZ311265
C 282	18.2	0.7	58	17	BH754616	BH754616 SALK_0429	C 355	18	0.6	60	17	AZ917459
C 283	18.2	0.7	59	9	AA071902	AA071902 mm71e04.r	C 356	18	0.6	60	17	CNS03C5T
C 284	18.2	0.7	59	10	AM278357	AM278357 s143a12.y	C 357	17.8	0.6	60	17	AM250894
C 285	18.2	0.7	59	17	AZ307737	AZ307737 1M0009E10	C 358	17.8	0.6	62	13	BJ045098
C 286	18.2	0.7	59	17	AZ311531	AZ311531 1M0027G03	C 359	17.8	0.6	62	17	AZ939796
C 287	18.2	0.7	59	17	AZ361084	AZ361084 1M0104D08	C 360	17.8	0.6	62	17	AT798406
C 288	18.2	0.7	60	9	AT965589	AT965589 sc74b04.y	C 361	17.8	0.6	63	9	AA445526
C 289	18.2	0.7	60	12	BF718477	BF718477 EST250.m1	C 362	17.8	0.6	63	14	R83676
C 290	18	0.6	38	10	AV847485	AV847485 AV847485	C 363	17.8	0.6	66	9	A1073981
C 291	18	0.6	44	17	AZ831947	AZ831947 2M0112B03	C 364	17.8	0.6	66	9	A1935210
C 292	18	0.6	46	9	AT624777	AT624777 ts44d09.x	C 365	17.8	0.6	66	46	AZ466375
C 293	18	0.6	46	9	AA625631	AA625631 ad10d01.s	C 366	17.8	0.6	66	48	AZ936691
C 294	18	0.6	46	17	AT763918	AT763918 Arabidops	C 367	17.8	0.6	49	17	AZ514513
C 295	18	0.6	48	17	AZ335856	AZ335856 1M0065C10	C 368	17.8	0.6	49	17	AZ586942
C 296	18	0.6	49	17	AT118170	AT118170 ue38f11.x	C 369	17.8	0.6	50	9	AU102796
C 297	18	0.6	49	17	BH641239	BH641239 1008046D0	C 370	17.8	0.6	50	9	AU103239
C 298	18	0.6	49	17	BH803392	BH803392 1008095H0	C 371	17.8	0.6	50	9	AU105409

[illegible]

Best Local Similarity 67.2%; Pred. No. 3.3e+03;
Matches 39; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1491 CAGCAGACACACTCAGGGGTTAAACCTTATGTCCTCGGATGGGGAGNGCT 1548

Db 58 CACCTGTATACGACTCGGGGAGAAACCTTCAAGTCCCGAGTCCGCAAGTCT 1

RESULT 6
LOCUS A1597270/c 58 bp mRNA linear EST 21-APR-1999

DEFINITION vi4d09.x1 Beddington mouse embryonic region Mus musculus cDNA
clone IMAGE:907601 3' similar to gb:x74855 M.musculus zfp-51 mRNA
for a zinc finger protein (MOUSE);, mRNA sequence.

ACCESSION A1597270
VERSION A1597270.1 GI:4606318

KEYWORDS EST.
SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 58)

AUTHORS

Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, J., Person
B., Waller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritzer
E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R. and Wilson, R.

Unpublished (1999)
The WashU-NCI Mouse EST Project 1999

TITLE

JOURNAL

COMMENT

Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

Email: mouseest@wustl.edu
This clone is available royalty-free through LINL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:528265

This clone was previously sequenced on the 5' end only, this new
data is from the 3' end
Possible reversed clone: polyT not found
Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 1.

FEATURES

source

1. 58

/organism="Mus musculus"

/strain="C57BL/6 x DBA"

/db_xref="taxon:10090"

/clone="IMAGE:907601"

/clone_lib="Beddington mouse embryonic region"

/sex="pooled"

/tissue_type="embryo"

/dev_stage="7.5dpc"

/lab_host="DH12S"

/note="Organ: whole embryo; Vector: pCMV-SPORT; Site_1:
SalI; Site_2: NotI; Cloned unidirectionally. Primer:
Oligo dT. Gastrulating embryos were collected at 7.5dpc
from C57BL/6 x DBA matings, excluding embryos that had
developed head folds and all extraembryonic tissues.
Average insert size: 1.3 kb (range: 0.5 - 3.0 kb).
Referenced in Development 121, 2479-2489 (1995)."

BASE COUNT

17 a 11 c 10 g 20 t

ORIGIN

Query Match

Best Local Similarity 66.7%; Score 26.6; DB 9; Length 58;
Matches 38; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1746 CAGAGACATTCATTCAGGGGAAAGCCTTTATGTCGAGGAGTGGCAGAGGTTT 1802

Db 57 CAGAGATTCATTCGAGGAAAGCCTTCAGAGTAGATGATGCGCAATCTTTT 1

RESULT 7
LOCUS AA902889

DEFINITION AA902889 46 bp mRNA linear EST 09-JUN-1998

o49g04.s1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:150186 3'
similar to TR:Q29294 Q29294 ZINC FINGER PROTEIN; , mRNA sequence.

AA902889
AA902889.1 GI:3038012

KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 46)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:

www.bio.llnl.gov/bhrp/image/image.html

Trace considered overall poor quality
Insert Length: 1180 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 1.

FEATURES

source

1. 46

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:150186"

/clone_lib="NCI_CGAP_Kid3"

/lab_host="DH10B"

/note="Organ: kidney; Vector: p773D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - Oligo(dT) primer,
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified p773 vector. mRNA
source: 2 pooled kidneys. Library went through one round
of normalization. Library constructed by Bento Soares and
M. Fatima Bonaldo."

BASE COUNT

11 a 19 c 13 g 3 t

ORIGIN

Query Match

Best Local Similarity 75.0%; Score 26.4; DB 9; Length 46;
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1560 TCAACCTTAACAACACGAGGTCACACAGGGGAGAAAGCC 1603

Db 2 TCGGACCTCACCACAGCAGCGGCGCAGCAGCGGCGAGAGCC 45

RESULT 8
LOCUS AAL16306

DEFINITION AAL16306 55 bp mRNA linear EST 30-NOV-1996

zn88c02.s1 Stragelene lung carcinoma 937218 Homo sapiens cDNA clone
IMAGE:565346 3' similar to SW:KR4_HUMAN P10075 HKR4 PROTEIN; , mRNA
sequence.

ACCESSION AAL16306

VERSION AAL16306.1 GI:1697533

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE AUTHORS	TITLE JOURNAL MEDLINE COMMENT	FEATURES Source	BASE COUNT ORIGIN	Query Match Best Local Similarity 60.0% Matches 33: Conservative 0: Mismatches 22: Indels 0: Gaps 0:
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, B., Holtman, M., Kucaba, T., Lacey, M., Le, M., Le, N., Mardis, E., McCrue, S., Morris, M., Parsons, J., Plange, C., Rifkin, L., Rohlfing, T., Schellander, K., Soares, M.B., Tan, F., Thierly-Weg, J., Trevaastis, J., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags	Genome Res. 6 (9), 807-828 (1996) 97044478	Location/Qualifiers 1. .55 /organism="Homo sapiens" /db_xref="GDB:4594411" /db_xref="taxon:9606" /clone="IMAGE:565346" /clone_lib="Stratagene lung carcinoma 937218" /tissue_type="lung carcinoma" /cell_line="NCI-H69" /dev_stage="cell line NCI-H69" /lab_host="SOLR (Kanamycin resistant)" /note="Organ: lung; Vector: pBluescript SK-; Site: 1: EcorRI /site_2: XhoI; Cloned unidirectionally. Primer: Oligo dr. Small cell carcinoma cell line NCI-H69 Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGACAG 3' -3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'"	11 a 12 c 11 g 11 t 10 others	
0Y	1050 TGGAAAGTCMAACCTGATCATCAGGAGGACACATCAGGGGAGAAACCTTATG 1104			
Db	55 TGGCGTCTGTCATCTCGNNNNAGCATNAGAGNNTTCTACATCAGGGGAGAAACCTATG 1			
RESULT 9 A2513479/c	45 bp DNA linear GSS 05-OCT-2000			
LOCUS	IM0359P21R Mouse 10kb plasmid UGCGIM library Mus musculus genom.c			
DEFINITION	clone UGCGIM0359P21 R, DNA sequence.			
ACCESSION	A2513479			
VERSION	A2513479.1 GI:10694795			
KEYWORDS	GSS.			
SOURCE	house mouse.			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	1 (bases 1 to 45) Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Petersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R.			
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb			
JOURNAL	plasmid inserts			
COMMENT	Unpublished (2000) contact: Robert B. Weiss University of Utah Genome Center			

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0359 row: P column: 21
Seq primer: CACACAGGAACAGCTATGACAC
Class: plasmid ends
High quality sequence stop: 45.
Location/Qualifiers
1. 45
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U08C1M0359P21"
/clone.lib="Mouse 10kb plasmid U08C1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1473211419b1AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbtp/image/image.html

Trace considered overall poor quality
 Insert Length: 1844 Std Error: 0.00
 Seq primer: 40m13 fwd. Fr from Amersham
 High quality sequence stop: 1.

FEATURES

Location/Qualifiers

1. .50
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1560174"
 /clone_lib="NCI_CGAP_CoB"
 /tissue_type="adenocarcinoma"
 /lab_host="DH10B"
 /note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a
 modified polylinker; 1st strand cDNA was prepared from
 colon adenocarcinoma, and was then primed with a Not I -
 oligo(dT) primer. Double-stranded cDNA was ligated to Eco
 RI adaptors (Pharmacia), digested with Not I and cloned
 into the Not I and Eco RI sites of the modified pT73
 vector. Library is normalized. Library was constructed by
 Bento Soares and M. Fatima Bernaldo."

BASE COUNT

5 a 15 c 21 g 9 t

ORIGIN

Query Match 0.9%; Score 24.4; DB 9; Length 50;
 Best Local Similarity 68.0%; Pred. No. 2.8e+04;
 Matches 34; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

OY 1658 GCACCAAGGACACCTCAGGAGAGACCATTTTGTGCTGCTG 1707

Db 50 GCACCAAGGACATCCACACGAGAGACCATTTTGTGCTGCTG 1

RESULT 11

R37288/c

LOCUS R37288 38 bp mRNA linear EST 04-MAY-1995
 DEFINITION yf67a06.s1 Soares infant brain INIB Homo sapiens CDNA clone
 IMAGE:27044 3' similar to gb:X16282_cds1 ZINC FINGER PROTEIN CLONE
 647 (HUMAN); mRNA sequence.

ACCESSION

R37288

KEYWORDS

EST.

ORGANISM

SOURCE

human.

Human.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 38)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman,
 M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,
 Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston,
 R., Williamson, A., Woldmann, P. and Wilson, R.

The Mashu-Mercer EST Project

Unpublished (1995)

CONTACT: Wilson RK

Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu

Insert Size: 690

High quality sequence starts: 1 High quality sequence stops: 1

Source: IMAGE Consortium, LLNL This clone is available royalty-free
 through LLNL; contact the IMAGE Consortium (info@image.llnl.gov)
 for further information. Trace considered overall poor quality

Insert Length: 690 Std Error: 0.00

Seq primer: 21m13

High quality sequence stop: 1.

Location/Qualifiers

FEATURES

Source

1. .59

/organism="Mus musculus"

/strain="129,C57BL/6J,FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:5337481"

/clone_lib="NCI_CGAP_Mam3"

/tissue_type="tumor, gross tissue"

/dev_stage="10 months"

/lab_host="DH10B"

/note="Organ: mammary; Vector: PCMV-SPORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Library constructed by Life Technologies. Investigators
 providing samples: Lotz Henninghausen/Chu-Xia Deng, NH
 Reference for transgenic model: Xu et al., Nature Genetics
 22, 37-43 (1999)."

source

1. .38
 /organism="Homo sapiens"
 /db_xref="GDB:399391"
 /db_xref="taxon:9606"
 /clone="IMAGE:27044"
 /clone_lib="Soares infant brain INIB"
 /sex="female"
 /dev_stage="73 days post natal"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: whole brain; Vector: Lactid BA; Site 1: Not
 I; Site 2: Hind III; 1st strand cDNA was primed with a Not
 I - oligo(dT) primer 15'
 AACTGGAAGAAATTCGCGCCGCGGAGATTTTGTGCTGCTG 3';
 double-stranded cDNA was ligated to Hind III adaptors
 (Pharmacia), digested with Not I and directionally cloned
 into the Not I and Hind III sites of the Lactid BA vector.
 Library went through one round of normalization. Library
 constructed by Bento Soares and M. Fatima Bernaldo."

BASE COUNT

10 a 12.c 5 g 10 t

ORIGIN

Query Match 0.9%; Score 23.8; DB 14; Length 38;
 Best Local Similarity 77.8%; Pred. No. 3.5e+04;
 Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1179 AAGCCTATGTGTCAGAGATGCGGAGGACTT 1214

Db 36 AAGCCTATGAGTGTATGATGTTGGAGGCTTT 1

RESULT 12

B1650525/c

LOCUS B1650525 59 bp mRNA linear EST 12-SEP-2001
 DEFINITION 603296901f1 NCI_CGAP_Mam3 Mus musculus CDNA clone IMAGE:5337481 5',
 mRNA sequence.

ACCESSION B1650525

KEYWORDS

EST.

ORGANISM

SOURCE

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 59)

NIH-MGC <http://mgi.nci.nih.gov/>.

Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.

Email: cga@bcrfemail.nih.gov

Tissue Procurement: Lotz Henninghausen Ph.D., Chu-Xia Deng Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LLM11857 row: a column: 02

High quality sequence stop: 57.

Location/Qualifiers

1. .59

/organism="Mus musculus"

/strain="129,C57BL/6J,FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:5337481"

/clone_lib="NCI_CGAP_Mam3"

/tissue_type="tumor, gross tissue"

/dev_stage="10 months"

/lab_host="DH10B"

/note="Organ: mammary; Vector: PCMV-SPORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Library constructed by Life Technologies. Investigators
 providing samples: Lotz Henninghausen/Chu-Xia Deng, NH
 Reference for transgenic model: Xu et al., Nature Genetics
 22, 37-43 (1999)."

BASE COUNT 13 a 13 c 23 g 10 t
ORIGIN
Query Match 0.9%; Score 23.8; DB 13; Length 59;
Best Local Similarity 72.1%; Pred. No. 4.7e+04;
Matches 31; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 699 GCACCTTCAGCCACCTGAGAACACAGCCGACGACGTCCA 741
Db 54 GCGCTTTCAGCCGCCCTCAGACGTGACGCTCGCAGTTCA 12
RESULT 13 46 bp mRNA linear EST 16-MAR-1998
AA867748
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
BASE COUNT 11 a 11 c 15 g 9 t
ORIGIN
Query Match 0.9%; Score 23.6; DB 9; Length 46;
Best Local Similarity 69.6%; Pred. No. 4.6e+04;

11 a 11 c 15 g 9 t

11 a 11 c 15 g 9 t

Matches 32; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 1760 AGGGAAAGCCCTTTATGTGACGAGGTGCGACAGATTCGG 1805
Db 1 AGGTGACAAAGCCGCCACAGTGTCTGAGTGTGCAAGGTTCCG 46
RESULT 14 49 bp mRNA linear EST 11-MAR-1998
AA227017
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
BASE COUNT 20 a 9 c 9 g 11 t
ORIGIN
Query Match 0.8%; Score 23.4; DB 9; Length 49;
Best Local Similarity 67.3%; Pred. No. 5.5e+04;
Matches 33; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
QY 1052 GAAGTCAACCTGATCAGACATGACAGACACTCAGGAGAACT 1100
Db 1 GAATGAAAGTCTTATGAAACATGAAATTCACACATGCTAGAACT 49
RESULT 15 60 bp mRNA linear EST 19-DEC-2000
BF638864
LOCUS
DEFINITION
ACCESSION
VERSION
BF638864
BF638864 1 GI:11903022

Query Match 0.8%; Score 22.8; DB 17; Length 56;
 Best Local Similarity 79.4%; Pred. No. 9.2e+04;
 Matches 27; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 2142 TCATACCTCATCAGACACGACGACACACAG 2175
 Db 9 TCATACGCGCATCAGACACCATCAGACTCTCAG 42

RESULT 20

BI963825/c

LOCUS 1655a07.x1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
 DEFINITION CDNA clone IMAGE:5671596 3', mRNA sequence.

ACCESSION

BI963825

VERSION

BI963825.1

KEYWORDS

EST.

SOURCE

ORGANISM

human.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

1 (bases 1 to 55)

AUTHORS

Melton, D., Brown, J., Kenty, G., Permut, A., Lee, C., Kaestner, K.,

Lemishka, T., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,

Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistein, A.,

Schmitt, A., Thelning, B., Ritter, E., Ronko, I., Bennett, J., Cardenas

M., Gibbons, M., McCann, R., Cole, R., Tsagaris, R., Williams, T.,

Jackson, Y. and Bowers, Y.

TITLE

Endocrine Pancreas Consortium

COMMENT

Unpublished (2000)

Other ESTs: 1655a07.y1

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,

MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Douglas Melton DNA sequencing by:

Washington University Genome Sequencing Center For information on

obtaining a clone please contact: Juliana Brown

(brownjefas.harvard.edu) This sequence now available from the IMAGE

consortium, for clone orders contact: info@image.llnl.gov.

Location/Qualifiers

1..55

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5671596"

/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"

/sex="Both"

/tissue_type="Islets of Langerhans"

/dev_stage="Adult"

/lab_host="DH10B"

/note="Organ: Pancreas; Vector: pSPOR1; Site: 1; Not 1;

Site: 2; Sal 1; Starting library kit (Life Technologies). cDNA

SuperScript Plasmid library (Life Technologies). cDNA

made by oligo-dT priming. Size-selected by column

fractionation: average insert size 1.08 kb. Library was

amplified once on solid support and plasmid DNA from

library was prepared. The library DNA was normalized by

method #4 from Bonaldo, Lennon, and Soares 1996 Genome

Research 6:791-806; 0.5 microgram single-stranded library

plasmid DNA was mixed with 5 micrograms PCR product

representing library inserts and hybridized to an EcoT of

20. Single-stranded (unhybridized) plasmids were isolated

by hydroxyapatite chromatography and used to make this

library."

BASE COUNT

ORIGIN

19 a 5 c 12 g 19 t

Query Match 0.8%; Score 22.6; DB 13; Length 55;

Best Local Similarity 68.9%; Pred. No. 1e+05;

Matches 31; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 2710 TCCCTTCACAGAGAGCTGTTCTTTCATCAATAATCTT 2754
 Db 54 TCCTTTCACAGTGTACATGTTTACTCACAATAAATCTT 10

RESULT 21

AA767515/c

LOCUS 044a03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1307788 3'
 DEFINITION similar to TR:Q15920 Q15920 DNA-BINDING PROTEIN; mRNA sequence.

ACCESSION

AA767515

VERSION

AA767515.1

KEYWORDS

EST.

SOURCE

ORGANISM

human.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

1 (bases 1 to 58)

AUTHORS

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP).

Tumor Gene Index

Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue procurement: Louis M. Staudt, M.D., Ph.D., David Altman,

Ph.D., Gerald Marti, M.D.

cDNA library preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

CDNA library arrayed by: Greg Lennon, Ph.D.

DNA sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. consortium/LLNL at:

www.bio.llnl.gov/btrp/image.html

Location/Qualifiers

1..58

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:1307788"

/clone_lib="NCI_CGAP_GCB1"

/tissue_type="germinal center B cell"

/lab_host="DH10B"

/note="Vector: pRT73D-Pac (Pharmacia) with a modified

polylinker. Site: 1; Not 1; Site: 2; Eco RI; 1st strand cDNA

was prepared from human tonsillar cells enriched for

germinal center B cells by flow sorting (CD20+, IgD-),

provided by Dr. Louis M. Staudt (NCI), Dr. David Altman

(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was

primed with a Not I - oligo(dT) primer

15'-GTATACCAATCTGAAGCGGCGGCGCCCTCATTTTTTTTTTTT-3'

[Pharmacia], digested with Not I and cloned into the Not I

and Eco RI sites of the modified pRT73 vector. Library

went through one round of normalization, and was

constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT

ORIGIN

10 a 13 c 15 g 20 t

Query Match 0.8%; Score 22.6; DB 9; Length 58;

Best Local Similarity 64.2%; Pred. No. 1.1e+05;

Matches 34; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 1571 CAACACGAGGCTACACAGCGGAGAGGACATTTGTATAGGAGTGG 1623

Db 56 CAACACGAGGCTACACAGCGGAGAGGACATTTGTATAGGAGTGG 4

JOURNAL
COMMENT

Unpublished (1999)
Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
The library was constructed by Claire Murphy, Brandi Chapelli, and Dr. James McCarter at Washington University, St. Louis. DNA Sequencing by: Washington University Genome Sequencing Center.

FEATURES

source

1..52

/organism="Ascaris suum"
/db_xref="taxon:6253"
/clone_lib="Ascaris suum male gut SL1 TOPO v1 Murphy
Chapelli McCarter"
/sex="Male"
/tissue_type="Intestine"
/dev_stage="Adult"
/lab_host="DH10B"
/note="Vector: pCRIT-TOPO (Invitrogen); Site_1: EcoRI;
Site_2: EcoRI. The library was constructed by Claire
Murphy, Brandi Chapelli, and Dr. James McCarter at
Washington University, St. Louis. Oligo(dT)-SL1 PCR based
library. Ascaris suum male intestine cDNA PCR products of
size >400 nucleotides containing SL1 on the 5' end and
oligo(dT) on the 3' end were non-directionally cloned
into pCRIT-TOPO(Invitrogen) following the TOPO TA cloning
protocol. Dissected nematode tissues were provided by Dr.
Alan Scott (ascott@jhsph.edu) of the School of Public
Hygiene and Public Health at John Hopkins University in
Baltimore, MD"

BASE COUNT 15 a 9 c 16 g 12 t
ORIGIN

Query Match 0.8%; Score 22.2; DB 13; Length 52;
Best Local Similarity 69.8%; Pred. No. 1.3e+05;
Matches 30; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1643 ATCAACCTGATCAGCAGACACACACTCAGGAGAG 1685
DB 7 ATCAACGCTGCTCATGTAAGAAGAGACAGATTCCAGTCAGAGAG 49

RESULT 25
AZ310125/c

LOCUS AZ310125 48 bp DNA linear GSS 29-SEP-2000
DEFINITION IM0018M20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0018M20 R, DNA sequence.

ACCESSION AZ310125
VERSION AZ310125.1 GI:10351801

KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 48)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0018 row: M column: 20
Seq primer: CACACGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 48.
Location/Qualifiers
1..48

FEATURES

source

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="UUGC1M0018M20"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (9147321149b1AE129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 3 a 19 c 16 g 10 t
ORIGIN

Query Match 0.8%; Score 22; DB 17; Length 48;
Best Local Similarity 67.4%; Pred. No. 1.4e+05;
Matches 31; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 162 GAGACCAGGAATGCTACAGGCTCTGAGAGCCAAAGAGG 207
DB 46 GGGACTCGGCCAGTGCTACAGGCCGCCGCCGACACAGAGAG 1

RESULT 26
A2665324/c

LOCUS A2665324 55 bp DNA linear GSS 14-DEC-2000
DEFINITION IM0546007R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0546007 R, DNA sequence.

ACCESSION A2665324
VERSION A2665324.1 GI:11802470

KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 55)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)⁺ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M. Fatima Bonaldo.

BASE COUNT 6 a 15 c 12 g 9 t 1 others

ORIGIN

Query Match 0.8%; Score 21.2; DB 9; Length 43;
Best Local Similarity 67.4%; Pred. No. 2.3e+05;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 1761 GGGGAAACCTTTATGTGACGAGGTGTGCACAAAGTTTC 1803
111 111 111 111 111 111 111 111 111 111
43 GGGAGAAACCTTCNAAGTCCCGGAGTGGCAGGCTTCC 1

RESULT 33
LOCUS R75644 49 bp mRNA linear EST 06-JUN-1995
DEFINITION Y159F01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone
IMAGE:143545 3' similar to SP:S40468 S40468 PROTEASOME SUBUNIT
RC10-II - ; mRNA sequence.
R75644
R75644.1 GI:850326

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 49)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston
R., Williamson, A., Wohldmann, P. and Wilson, R.
The Washu-Merck EST Project
Unpublished (1995)

TITLE
JOURNAL
COMMENT

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estelw@wustl.edu
Insert Size: 848
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone; similarity on wrong strand
Insert length: 848 Std Error: 0.00
Seq primer: Promega -21ml3
High quality sequence stop: 1.
Location/Qualifiers

FEATURES

1. 49
/organism="Homo sapiens"
/db_xref="GDB:552718"
/db_xref="taxon:9606"
/clone="IMAGE:143545"
/clone_lib="Soares placenta Nb2HP"
/sex="Female"
/dev_stage="placenta obtained at birth (full term)"
/lab_host="PH10B (ampicillin resistant)"
/note="Organ: placenta; Vector: pT73D (Pharmacia) with a
modified polylinker; Site: 1; Not I; Site: 2; Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
AAGTGGAGAAATTCGGCGCGAGGAAATTTTATTTTATTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo.

BASE COUNT 11 a 12 c 10 g 14 t 2 others

ORIGIN

Query Match 0.8%; Score 21.2; DB 14; Length 49;
Best Local Similarity 72.2%; Pred. No. 2.6e+05;
Matches 26; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 1174 GGCTCAACCTTATGTGCAAGAAATGTGGCACA 1209
111 111 111 111 111 111 111 111 111 111
45 GGCTGAACCTGTATNAGTNAAGCAAGTCGCGACA 10

RESULT 34
LOCUS AUI05724/c 50 bp mRNA linear EST 30-AUG-2001
DEFINITION AUI05724 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone.
KAT10272, mRNA sequence.
AUI05724
AUI05724.1 GI:13555245

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)

TITLE
JOURNAL
COMMENT

Contact: Yutaka Suzuki
Department of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
Source
1. 50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="KAT10272"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylfluninate treated U937 cells"
Location/Qualifiers

BASE COUNT 7 a 6 c 17 g 20 t

Query Match 0.8%; Score 21.2; DB 9; Length 50;
Best Local Similarity 64.0%; Pred. No. 2.6e+05;
Matches 32; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

OY 584 AGATCAGAAACACAGAGATCATTCCTTTAGTGGCAAGCAGAT 633
111 111 111 111 111 111 111 111 111 111
50 AAGACACATCAACAGCGCGACACTGATGATTCACCAAAAT 1

RESULT 35
LOCUS B02962 51 bp DNA linear GSS 13-JUL-1996
DEFINITION CSRL-164B7-u CSRL flow sorted Chromosome 11 specific cosmid Homo
sapiens genomic clone CSRL-164B7, DNA sequence.
ACCESSION B02962
VERSION B02962.1 GI:1412240
KEYWORDS GSS.
SOURCE human.

```

Email: radixon@noble.org
Insert Length: 923      Std Error: 0.00
Plate: 048 row: A column: 11
Seq primer: TCACACAGCAAGACGCTATGAC.
Location/Qualifiers
1. 52
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="MF048A11ST"
/clone_lib="Developing stem"
/tissue_type="stem"
/dev_stage="Pooled developmental"
/notes="Vector: lambda zap; Contains a mixture of
internodal stem segments"
BASE COUNT
14 a 16 c 2 g 20 t
ORIGIN
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Query Match 0.8%; Score 21.2; DB 10; Length 52;
Best Local Similarity 69.0%; Pred. No. 2.7e+05;
Matches 29; Conservative 0; Mismatches 13; Indels 0; Gaps 0

OY 321 CTGCTCTCAGTCGGAATTCATCTCTTAAACCAAACTCAT 362
11 111 1 11 1111 11111111 11
Db 6 CTTCCTTCATCACTTGCACTTGCACTTCACCAAAACCTTT 47

RESULT 37
LOCUS A2595836/c 40 bp DNA linear GSS 13-DEC-2000
DEFINITION M04080808R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION clone UUGC1M040808 R, DNA sequence.
A2595836
VERSION A2595836.1 GI:11718026
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 40)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamll,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffoldling with paired end reads from 10kb
plasmid insets
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0408 row: 0 column: 08
Seq primer: CACACAGCAAGACGCTATGAC
Class: Plasmid ends
High quality sequence stop: 40.
location/Qualifiers
1. 40
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0408008"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: PMD29v; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hybridized to a 10kb

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FEATURES
source
Location/Qualifiers
1. .50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="INEC0029"
/note="Differential display comparison of untreated and dimethylfluminate treated U937 cells"

BASE COUNT
13 a 8 c 17 g 12 t

ORIGIN

Query Match 0.8% Score 21; DB 9; Length 50;
Best Local Similarity 73.0%; Pred. No. 3e+05;
Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Db 99 CGGCGTGCACCCGCTTCATCTCTCTTGACACTT 135
50 CGGCGGCGACGACACTCAATTTCTTTCAGACTT 14

RESULT 41
AA976008/c 58 bp mRNA linear EST 23-JUL-1998
LOCUS oq29b04.s1 NCI-CGAP-GC4 Homo sapiens cDNA clone IMAGE:1587727 3.
DEFINITION similar to SW:ZM27_HUMAN P17033 ZINC FINGER PROTEIN 27 ;, mRNA
sequence.
ACCESSION AA976008
VERSION AA976008.1 GI:3151800
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 58)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rt@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 453 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. .58
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1587727"
/clone_11b="NCI-CGAP-GC4"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/note="Vector: pRTT3D-Pac (Pharmacia) with a modified
polylinker. 1st strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pRTT3
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldio."

BASE COUNT
15 a 15 c 15 g 13 t

ORIGIN

Query Match 0.8% Score 21; DB 9; Length 58;

Best Local Similarity 62.3%; Pred. No. 3.3e+05;
Matches 33; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Db 1677 GGGAGAACCCATTGTATGTGCGTGGAGGAGGCTTATATGTAAGTC 1729
58 GGAGGAACGCCCTATACGTTGTATGCGGTGGAAGAACCTTCATTCATGCTC 6

RESULT 42
AV957851 49 bp mRNA linear EST 14-MAR-2002
LOCUS AV957851 Nori Satoh unpublished cDNA library, egg ciona
DEFINITION intestinalis cDNA clone c1eg09a19 5', mRNA sequence.
ACCESSION AV957851
VERSION AV957851.1 GI:19446150
KEYWORDS EST.
SOURCE Ciona intestinalis.
ORGANISM Ciona intestinalis.
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Clonidae; Ciona.
1 (bases 1 to 49)
Satoh,N., Satou,Y., Kohara,Y. and Shin-I,T.
Expressed genes in ciona intestinalis
Unpublished (2000)
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
1. .49
/organism="Ciona intestinalis"
/db_xref="taxon:7719"
/clone="c1eg09a19"
/clone_11b="Nori Satoh unpublished cDNA library, egg"
/tissue_type="whole animal"
/dev-stage="egg"
/note="Vector: pBluescript SK"

BASE COUNT
24 a 7 c 10 g 8 t

ORIGIN

Query Match 0.8% Score 20.8; DB 10; Length 49;
Best Local Similarity 70.0%; Pred. No. 3.4e+05;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Db 2348 GGTCAAGTATGATGTGCGAGGAGCAATGATCCCA 2387
2 GCTCAGGTGTGATGATGACAGCAAGTCAAAATCCAA 41

RESULT 43
AZ666147/c 56 bp DNA linear GSS 14-DEC-2000
LOCUS 1M0548C04F Mouse 10kb plasmid UUCGIM library Mus musculus genomic
DEFINITION clone UUCG1M0548C04 F, DNA sequence.
ACCESSION AZ666147
VERSION AZ666147.1 GI:11803293
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 56)
Dunn,D., Aoyagi,A., Barber,M., Baecorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss

JOURNAL
COMMENT


```

/tissue.type="mammary adenocarcinoma, cell line"
/lab.host="DH10B (phage-resistant)"
/notes="Organ: breast; Vector: pCMV-SPORT6; Site: 1: NotI,
Site: 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT
  9 a      13 c      20 g      10 t
Query Match
  0.7%; Score 20.6; DB 12; Length 52;
  Best Local Similarity 62.7%; Pred. No. 4e+05;
  Matches 32; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 2322 CCGTGGATGCTGGTGTGGAACCGGTCAGTATGATGCGCAGAG 2372
  11 1111 11 1111 11 11111111 11 11 111
  2 CCGTGGACGGGTGGTTGGACAACACATCAGTCTGGAGCTGGCGCAG 52

RESULT 46
TA328D010/c
LOCUS TA328D010 52 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 328d01, reverse sequence.
ACCESSION AL491514
VERSION AL491514.1 GI:11868011
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei.
REFERENCE 1 (bases 1 to 52)
  Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
  Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
  Melville, S.E., Rajandream, M.A. and Barrell, B.G.
  Direct Submission
  Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
  project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
  Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
  nh@sanger.ac.uk
  Constructed at the Institute for Genomic Research (TIGR),
  Rockville, MD. Genomic DNA isolated from a cloned population of
  Trypanosoma brucei (TREU927/4 Gumat 10.1) was mechanically sheared
  to give a tight size distribution (
  4 kb). The v+1 method used for the library construction is
  described in detail in Smith, H. and Venter, J.C. (Making small
  insert libraries for whole genome shotgun sequencing projects. In
  Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
  Barrell, Oxford University Press, 1999).
  Email: nelsayed@tigr.org
  Details of T. brucei sequencing at the Sanger Centre are available
  at http://www.sanger.ac.uk/projects/T_brucei/.
  Location/Qualifiers
    1..52
      /organism="Trypanosoma brucei"
      /strain="TREU927"
      /db_xref="taxon:5691"
      /clone="328d01"
      16 c      7 g      16 t

BASE COUNT
  13 a      16 c      7 g      16 t
ORIGIN
Query Match
  0.7%; Score 20.6; DB 17; Length 52;
  Best Local Similarity 67.4%; Pred. No. 4e+05;
  Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 2076 CAGAGACACACATGAGTATGATGATGATGATGATGAT 2118
  11 1111 11 1111 1111 1111 1111 1111 1111
  43 CCGGGGCGATCTTCAGGAAGAATATATATATATATATATAT 1

Db 43 CCGGGGCGATCTTCAGGAAGAATATATATATATATATATAT 1

RESULT 47
AA494740
LOCUS AA494740 55 bp mRNA linear EST 27-JUN-1997

```

```

DEFINITION fall10.r1 zebrafish ICRFzfls Danio rerio cDNA clone 14h24 5'
  similar to SW:2658_XENLA P18730 GASTRULA ZINC FINGER PROTEIN
  XLOC58.1; mRNA sequence.
ACCESSION AA494740
VERSION AA494740.1 GI:2225168
KEYWORDS EST.
SOURCE zebrafish.
ORGANISM Danio rerio
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
  ; Cyprinidae; Danio.
  1 (bases 1 to 55)
  Clark, M., Lehrach, H., Appel, B., Eisen, J., Johnson, S., Marra, M.,
  Eddy, S., Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisler, G.,
  Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Martin, J., Moore, B.,
  Schellenberg, K., Steptoe, M., Tan, F., Theisling, B., White, Y., Wylie
  , T., Waterston, R. and Wilson, R.
  WashU Zebrafish EST Project
  Unpublished (1997)
  Contact: Steve Johnson
  Washington University School of Medicine
  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: est@wustl.edu
  Steve Johnson lab internal ID - P3_284 NOTE - For this library, the
  CLONE id field represents a position identifier on the original
  cDNA library preparation plate. cDNA library preparation: Matthew
  Clark. cDNA library arrayed by: Matthew Clark. DNA sequencing by:
  Genome Systems, St. Louis, and Max Planck Institut fuer Molekulare
  Genetik, Berlin Tel +49 30 84 13 1235
  Trace considered overall poor quality
  Possible reversed clone: similarity on wrong strand
  Seq primer: 77 bp from Amersham
  High quality sequence stop: 1.
  Location/Qualifiers
    1..55
      /organism="Danio rerio"
      /db_xref="taxon:7955"
      /clone="14h24"
      /clone_lib="zebrafish ICRFzfls"
      /sex="mixed"
      /tissue_type="pooled 26-somite embryos"
      /lab_host="XLI-blue MRF"
      /note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; 1st
      strand cDNA was primed with a Not I - oligo(dT)15 primer
      15'pGACTAGTTCTAGATCGGACGCGCCGCTTTTCTTTTCTTTT3', on
      mRNA from pooled 26 somite zebrafish embryos;
      double-stranded cDNA was ligated to Sal I adaptors (BRL),
      digested with Not I and cloned into the Not I and Sal I
      sites of the pSPORT1 vector (BRL). Library was constructed
      by Matthew Clark (Lehrach lab; ICRF, London and Max
      Planck Institut fuer Molekulare Genetik, Berlin) and was
      not biochemically normalised. 70,000 clones from this
      library were arrayed on high density filters and
      subsequently screened by oligonucleotide hybridization
      fingerprinting to identify unique or minimally redundant
      clones for more intensive analysis."

BASE COUNT
  16 a      16 c      13 g      10 t
ORIGIN
Query Match
  0.7%; Score 20.6; DB 9; Length 55;
  Best Local Similarity 62.7%; Pred. No. 4.2e+05;
  Matches 32; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1407 CACTTAAGACACACAGACAGACCCCTTATGTATGACAGATGTGG 1457
  111 11 11 11 1111 111 11 11 111111111
  2 CACATTAAATCCAAACGTGGAGCAACCCCTTACCTGACCTGATGTGG 52

RESULT 48
BH862808/c

```



```

/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0564L13"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-."
/notes="Vector: PMD42uv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g11473211419b1AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT      6 a      13 c      20 g      11 t
ORIGIN

```

```

Query Match      0.7%; Score 20.4; DB 17; Length 50;
Best Local Similarity 65.2%; Pred. No. 4.5e+05;
Matches 30; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
QY      2652 TCAGCTGCAGTAGAGAGAAATCACCCCTGCTGTGAGGTTGGGGA 2697
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      1 TCAGGTGCTGTAGGACACCTGACCCCTGCTGTGAGGTTGGGGA 46

```

Search completed: June 4, 2003, 10:24:23
Job time : 3924 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 4, 2003, 05:31:36 ; Search time 610 Seconds
(without alignments)
10233.671 Million cell updates/sec

Title: US-09-898-556a-3

Perfect score: 2772
Sequence: 1 cagcgcgtaagctggtg.....ttctaccatctccacct 2772

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 2274872

Minimum DB seq length: 0
Maximum DB seq length: 60

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : N.Geneseq_101002.*
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2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	2.2	60	24	ABN34034
2	49.4	1.8	51	23	ABL00474
3	49.4	1.8	51	23	ABL00878
4	35	1.3	60	24	ABN33915
5	34.6	1.2	51	22	AA177643
6	33.6	1.2	51	22	AA176919
7	33	1.2	51	22	AA177642
8	31.6	1.1	51	22	AA126920
9	31	1.1	60	24	ABN33655

10	30.6	1.1	60	24	ABN34117	Human spliced tran
11	29.6	1.1	60	24	ABN34244	Human spliced tran
12	28.6	1.0	60	24	ABN34405	Human spliced tran
13	28.6	1.0	60	24	ABN47634	Human spliced tran
14	27.6	1.0	51	22	AA179453	Human silent SNP c
15	27.6	1.0	51	22	AA178093	Human silent SNP c
16	27	1.0	60	24	AA178093	Human silent SNP c
17	26.8	1.0	51	22	AA178093	Human silent SNP c
18	26.8	1.0	51	22	AA178093	Human silent SNP c
19	26.6	1.0	51	22	AA178093	Human silent SNP c
20	26.6	1.0	51	22	AA178093	Human silent SNP c
21	26.6	1.0	51	22	AA178093	Human silent SNP c
22	26.6	1.0	51	22	AA178093	Human silent SNP c
23	26.2	0.9	51	22	AA178093	Human silent SNP c
24	26	0.9	51	22	AA178093	Human silent SNP c
25	25.8	0.9	60	24	AA178093	Human silent SNP c
26	25.6	0.9	60	24	AA178093	Human silent SNP c
27	25.6	0.9	60	24	AA178093	Human silent SNP c
28	25.4	0.9	60	24	AA178093	Human silent SNP c
29	25.2	0.9	60	24	AA178093	Human silent SNP c
30	25.2	0.9	60	24	AA178093	Human silent SNP c
31	25.2	0.9	60	24	AA178093	Human silent SNP c
32	25.2	0.9	60	24	AA178093	Human silent SNP c
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34	25	0.9	60	24	AA178093	Human silent SNP c
35	24.8	0.9	60	24	AA178093	Human silent SNP c
36	24.8	0.9	60	24	AA178093	Human silent SNP c
37	24.8	0.9	60	24	AA178093	Human silent SNP c
38	24.6	0.9	60	24	AA178093	Human silent SNP c
39	24.6	0.9	60	24	AA178093	Human silent SNP c
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41	24.6	0.9	60	24	AA178093	Human silent SNP c
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43	24.6	0.9	60	24	AA178093	Human silent SNP c
44	24.6	0.9	60	24	AA178093	Human silent SNP c
45	24.4	0.9	60	24	AA178093	Human silent SNP c
46	24.4	0.9	60	24	AA178093	Human silent SNP c
47	24.4	0.9	60	24	AA178093	Human silent SNP c
48	23.8	0.9	60	24	AA178093	Human silent SNP c
49	23.8	0.9	60	24	AA178093	Human silent SNP c
50	23.8	0.9	60	24	AA178093	Human silent SNP c
51	23.8	0.9	60	24	AA178093	Human silent SNP c
52	23.8	0.9	60	24	AA178093	Human silent SNP c
53	23.8	0.9	60	24	AA178093	Human silent SNP c
54	23.6	0.9	60	24	AA178093	Human silent SNP c
55	23.6	0.9	60	24	AA178093	Human silent SNP c
56	23.4	0.8	60	24	AA178093	Human silent SNP c
57	23.2	0.8	60	24	AA178093	Human silent SNP c
58	23	0.8	60	24	AA178093	Human silent SNP c
59	23	0.8	60	24	AA178093	Human silent SNP c
60	23	0.8	60	24	AA178093	Human silent SNP c
61	23	0.8	60	24	AA178093	Human silent SNP c
62	23	0.8	60	24	AA178093	Human silent SNP c
63	23	0.8	60	24	AA178093	Human silent SNP c
64	22.8	0.8	60	24	AA178093	Human silent SNP c
65	22.8	0.8	60	24	AA178093	Human silent SNP c
66	22.6	0.8	60	24	AA178093	Human silent SNP c
67	22.4	0.8	60	24	AA178093	Human silent SNP c
68	22.4	0.8	60	24	AA178093	Human silent SNP c
69	22.4	0.8	60	24	AA178093	Human silent SNP c
70	22.4	0.8	60	24	AA178093	Human silent SNP c
71	22.4	0.8	60	24	AA178093	Human silent SNP c
72	22.2	0.8	60	24	AA178093	Human silent SNP c
73	22.2	0.8	60	24	AA178093	Human silent SNP c
74	22.2	0.8	60	24	AA178093	Human silent SNP c
75	22.2	0.8	60	24	AA178093	Human silent SNP c
76	22.2	0.8	60	24	AA178093	Human silent SNP c
77	22.2	0.8	60	24	AA178093	Human silent SNP c
78	22.2	0.8	60	24	AA178093	Human silent SNP c
79	22.2	0.8	60	24	AA178093	Human silent SNP c
80	22	0.8	60	24	AA178093	Human silent SNP c
81	21.8	0.8	60	24	AA178093	Human silent SNP c
82	21.8	0.8	60	24	AA178093	Human silent SNP c

83	21.8	0.8	60	24	ABN34039	Human spliced tran
84	21.8	0.8	60	24	ABN34100	Human spliced tran
85	21.8	0.8	60	24	ABA03561	Relaxin/IGF/insull
86	21.6	0.8	41	13	AAO26571	Triplex PCR primer
87	21.6	0.8	41	24	ABA05347	Human zinc finger
88	21.6	0.8	60	24	ABN33990	Human spliced tran
89	21.4	0.8	31	22	AAI30914	Human single nucle
90	21.4	0.8	50	22	AAI32254	Human SNP oligonu
91	21.4	0.8	51	22	AAI76047	Human silent SNP c
92	21.4	0.8	60	24	ABN36823	Human spliced tran
93	21.4	0.8	60	24	ABN48558	Human spliced tran
94	21.4	0.8	60	24	AAI29929	Human spliced tran
95	21.2	0.8	50	22	AAI27943	T-wt oligonucleoti
96	21.2	0.8	50	22	AAI75119	Human SNP oligonc
97	21.2	0.8	50	22	AAI75119	Human silent SNP c
98	21.2	0.8	60	24	ABN36408	Human probe #8. H
99	21.2	0.8	60	24	ABN33725	Human spliced tran
100	21.2	0.8	60	24	ABN33725	Human spliced tran
101	21.2	0.8	60	24	ABN34378	Human spliced tran
102	21.2	0.8	40	21	AAI32253	Human spliced tran
103	21.2	0.8	45	24	AAI32253	Thimline responsiv
104	21.2	0.8	49	17	AAI35402	Three finger DNA a
105	21.2	0.8	50	22	AAI35402	Primer MS-P2 to c
106	21.2	0.8	50	22	AAI32253	S. capricanis smel
107	21.2	0.8	59	18	AAI75984	Human SNP oligonc
108	21.2	0.8	60	24	ABN40788	Truncated P-select
109	21.2	0.8	60	24	ABN48819	Human spliced tran
110	20.8	0.8	60	24	ABN50298	Human spliced tran
111	20.8	0.8	33	22	AAH43217	Human zinc finger
112	20.8	0.8	41	22	AAH76682	Human zinc finger
113	20.8	0.8	41	22	AAI42068	Novel murine zinc
114	20.8	0.8	48	16	AAO87598	Primer for PCR ampl
115	20.8	0.8	48	16	AAO85335	PCR primer fragmen
116	20.8	0.8	51	22	AAI27314	Human SNP oligonc
117	20.8	0.8	51	23	ABU00548	Human silent nonco
118	20.8	0.8	60	24	ABN33735	Human spliced tran
119	20.8	0.8	60	24	ABN33917	Human spliced tran
120	20.8	0.8	60	24	ABN43176	Human spliced tran
121	20.8	0.8	60	24	ABN44593	Human spliced tran
122	20.6	0.7	47	24	ABN48210	Human spliced tran
123	20.6	0.7	47	24	ABN71743	Human spliced tran
124	20.6	0.7	51	22	AAI28100	Streptococcus agal
125	20.6	0.7	51	22	AAI29371	Human SNP oligonc
126	20.6	0.7	51	22	AAI78540	Human silent SNP c
127	20.6	0.7	51	22	AAI78541	Human silent SNP c
128	20.6	0.7	52	18	AAI57992	Truncated P-select
129	20.6	0.7	60	24	ABN33972	Human spliced tran
130	20.6	0.7	60	24	ABN33532	Human spliced tran
131	20.6	0.7	60	24	ABN35918	Human spliced tran
132	20.6	0.7	60	24	ABN38523	Human spliced tran
133	20.6	0.7	60	24	ABN50535	Human spliced tran
134	20.4	0.7	41	24	ABA98015	Human superoxide d
135	20.4	0.7	41	24	ABA04288	Human sex determin
136	20.4	0.7	45	21	AAZ96671	T cell antigen rec
137	20.4	0.7	50	22	AAI29955	Human SNP oligonc
138	20.4	0.7	51	22	AAI27636	Human SNP oligonc
139	20.4	0.7	51	22	AAI74659	Human silent SNP c
140	20.4	0.7	54	20	AAV84652	PCR primer used to
141	20.4	0.7	60	24	ABN32547	Human spliced tran
142	20.4	0.7	60	24	ABN38013	Human spliced tran
143	20.4	0.7	60	24	ABN39542	Human spliced tran
144	20.4	0.7	60	24	ABN40506	Human spliced tran
145	20.4	0.7	60	24	ABN42336	Human spliced tran
146	20.4	0.7	60	24	ABN43789	Human spliced tran
147	20.4	0.7	60	24	ABN44217	Human spliced tran
148	20.4	0.7	60	24	ABN44689	Human spliced tran
149	20.4	0.7	60	24	ABN48107	Human spliced tran
150	20.2	0.7	60	24	ABN50256	Human spliced tran
151	20.2	0.7	41	24	ABA03772	Human zinc finger
152	20.2	0.7	41	24	ABA05348	Human zinc finger
153	20.2	0.7	47	21	AAZ65854	Human map-related
154	20.2	0.7	50	15	AAO70985	PCNA gene specific
155	20.2	0.7	50	15	AAI28938	Human SNP oligonc
			51	22	AAI28074	Human SNP oligonc
156	20.2	0.7	51	22	AAI30203	Human SNP oligonc
157	20.2	0.7	60	19	AAV19098	Synthetic Streptom
158	20.2	0.7	60	19	AAV18002	PCR primer used to
159	20.2	0.7	60	24	AAO37838	Human FAII transme
160	20.2	0.7	60	24	ABN32242	Human spliced tran
161	20.2	0.7	60	24	ABN33459	Human spliced tran
162	20.2	0.7	60	24	ABN34836	Human spliced tran
163	20.2	0.7	60	24	ABN42196	Human spliced tran
164	20.2	0.7	60	24	ABN46051	Human spliced tran
165	20.2	0.7	60	24	ABN47576	Human spliced tran
166	20.2	0.7	60	24	ABN48331	Human spliced tran
167	20.2	0.7	60	24	ABN48650	Human spliced tran
168	20.2	0.7	41	24	ABL40933	Human zinc finger
169	20.2	0.7	42	20	AAI388615	Human chromosome 1
170	20.2	0.7	44	12	AAO12365	Probe I3 based on
171	20.2	0.7	44	13	AAO35070	Probe I3 for detec
172	20.2	0.7	47	21	AAZ69441	Human map-related
173	20.2	0.7	48	16	AAO81434	HBV target sequenc
174	20.2	0.7	50	19	AAV30378	Oligomer p50rg16 u
175	20.2	0.7	50	24	AAI35532	Methylomonas 16a s
176	20.2	0.7	51	21	AAI77399	Human clone CG4492
177	20.2	0.7	51	22	AAI27337	Human SNP oligonc
178	20.2	0.7	52	22	AAH91974	Human inflammatory
179	20.2	0.7	54	20	AAI21943	Fragment of the VD
180	20.2	0.7	55	21	AAI65685	Human BPI PCR prim
181	20.2	0.7	60	24	ABN33155	Human spliced tran
182	20.2	0.7	60	24	ABN33264	Human spliced tran
183	20.2	0.7	60	24	ABN33445	Human spliced tran
184	20.2	0.7	60	24	ABN33716	Human spliced tran
185	20.2	0.7	60	24	ABN33813	Human spliced tran
186	20.2	0.7	60	24	ABN34721	Human spliced tran
187	20.2	0.7	60	24	ABN37226	Human spliced tran
188	20.2	0.7	60	24	ABN37979	Human spliced tran
189	20.2	0.7	60	24	ABN39834	Human spliced tran
190	20.2	0.7	60	24	ABN42034	Human spliced tran
191	20.2	0.7	60	24	ABN43740	Human spliced tran
192	20.2	0.7	60	24	ABN46638	Human spliced tran
193	20.2	0.7	60	24	ABN48545	Human spliced tran
194	19.8	0.7	28	21	AAA38456	Murine SM22 gene C
195	19.8	0.7	28	21	AAZ93777	CARG Element of de
196	19.8	0.7	41	24	ABK48079	Human zinc-finger
197	19.8	0.7	41	24	ABK48080	Human zinc-finger
198	19.8	0.7	47	19	AAI28740	Oligonucleotide SM
199	19.8	0.7	47	22	AAI27621	Oligo SME-1, used
200	19.8	0.7	47	22	AAI20575	Oligo SME-1, used 1
201	19.8	0.7	47	22	AAI26589	Mouse SM22-alpha p
202	19.8	0.7	47	24	ABK40917	Human obesity-asso
203	19.8	0.7	47	24	ABK33341	Electrophoretic mo
204	19.8	0.7	50	22	AAI30970	Human SNP oligonc
205	19.8	0.7	50	22	AAI76271	Human silent SNP c
206	19.8	0.7	51	22	AAI27049	Human SNP oligonc
207	19.8	0.7	51	22	AAI74524	Human silent SNP c
208	19.8	0.7	51	22	AAI74524	Human silent SNP c
209	19.8	0.7	51	22	AAI76039	Human silent SNP c
210	19.8	0.7	51	22	AAI76566	Human silent SNP c
211	19.8	0.7	51	23	ABL00876	Human amino acid c
212	19.8	0.7	57	20	AAO32335	PCR primer used to
213	19.8	0.7	58	21	AAI31951	Human secreted pro
214	19.8	0.7	59	20	AAI22491	Oligonucleotide se
215	19.8	0.7	60	16	AAO98853	Anti-human IL-4 hu
216	19.8	0.7	60	18	AAV75972	Staphylococcus aur
217	19.8	0.7	60	24	ABN32367	Human spliced tran
218	19.8	0.7	60	24	ABN33529	Human spliced tran
219	19.8	0.7	60	24	ABN34919	Human spliced tran
220	19.8	0.7	60	24	ABN35263	Human spliced tran
221	19.8	0.7	60	24	ABN43641	Human spliced tran
222	19.8	0.7	60	24	ABN44277	Human spliced tran
223	19.8	0.7	60	24	ABN45332	Human spliced tran
224	19.8	0.7	60	24	ABN46381	Human spliced tran
225	19.8	0.7	60	24	ABN47162	Human spliced tran
226	19.8	0.7	60	24	ABN49599	Human spliced tran
227	19.8	0.7	60	24	ABN49864	Human spliced tran
228	19.8	0.7	60	24	ABN50011	Human spliced tran

C 375	19	0.7	45	24	ABAD1543	MyCamtrose biosyrit
C 376	19	0.7	46	22	AAD19782	Human ST drug-meta
C 377	19	0.7	48	22	AAD33621	OTS-008 primer use
C 378	19	0.7	48	24	ABK22526	Human ERG ambrzym
C 379	19	0.7	50	11	AAO06711	HBV LRA2C.75 amp1
C 380	19	0.7	50	20	AAK53307	Probe used to Isol
C 381	19	0.7	50	21	AAAS4096	Probe for PRO228 c
C 382	19	0.7	50	21	AAZ93456	Prob for PRO228 cD
C 383	19	0.7	50	22	AAAL33956	Human SNP oligonuc
C 384	19	0.7	50	22	AAAL34154	Human SNP oligonuc
C 385	19	0.7	50	22	AAAF72465	Human PRO polypt
C 386	19	0.7	50	22	AAAC97436	Human PRO228 hyd:1
C 387	19	0.7	51	22	AAAL27615	Human SNP oligonuc
C 388	19	0.7	51	22	AAAL28103	Human SNP oligonuc
C 389	19	0.7	51	22	AAAL28592	Human SNP oligonuc
C 390	19	0.7	51	22	AAAL29235	Human SNP oligonuc
C 391	19	0.7	51	22	AAAL32937	Human SNP oligonuc
C 392	19	0.7	51	22	AAAL33010	Human SNP oligonuc
C 393	19	0.7	51	22	AAAL74758	Human silent SNP c
C 394	19	0.7	51	22	AAAL76764	Human silent SNP c
C 395	19	0.7	51	22	AAAL78672	Human silent SNP c
C 396	19	0.7	51	22	AAAL79706	Human conservative
C 397	19	0.7	51	22	AAAH96607	Human DNA containi
C 398	19	0.7	51	22	AAAH96616	Human SNP flanki ng
C 399	19	0.7	51	23	ABLU00455	Human silent nonco
C 400	19	0.7	54	17	AAAT34305	Primer NOTKINCYS f
C 401	19	0.7	55	21	AAAC29085	Human secreted pro
C 402	19	0.7	57	17	AAAT28358	HCV primer used in
C 403	19	0.7	59	21	AAAT26824	S. cerevisiae gene
C 404	19	0.7	60	22	AAAF1238	Novel BAC vector c
C 405	19	0.7	60	24	ABN33712	Human spliced tran
C 406	19	0.7	60	24	ABN33743	Human spliced tran
C 407	19	0.7	60	24	ABN34130	Human spliced tran
C 408	19	0.7	60	24	ABN34393	Human spliced tran
C 409	19	0.7	60	24	ABN35543	Human spliced tran
C 410	19	0.7	60	24	ABN36348	Human spliced tran
C 411	19	0.7	60	24	ABN36684	Human spliced tran
C 412	19	0.7	60	24	ABN36837	Human spliced tran
C 413	19	0.7	60	24	ABN38197	Human spliced tran
C 414	19	0.7	60	24	ABN39382	Human spliced tran
C 415	19	0.7	60	24	ABN40173	Human spliced tran
C 416	19	0.7	60	24	ABN40163	Human spliced tran
C 417	19	0.7	60	24	ABN42743	Human spliced tran
C 418	19	0.7	60	24	ABN42984	Human spliced tran
C 419	19	0.7	60	24	ABN43567	Human spliced tran
C 420	19	0.7	60	24	ABN44449	Human spliced tran
C 421	19	0.7	60	24	ABN45251	Human spliced tran
C 422	19	0.7	60	24	ABN46757	Human spliced tran
C 423	19	0.7	60	24	ABN46802	Human spliced tran
C 424	19	0.7	60	24	ABN46969	Human spliced tran
C 425	19	0.7	60	24	ABN46995	Human spliced tran
C 426	19	0.7	60	24	ABN47943	Human spliced tran
C 427	19	0.7	60	24	ABN49054	Human spliced tran
C 428	19	0.7	60	24	ABN49123	Human spliced tran
C 429	19	0.7	60	24	ABN50617	Human spliced tran
C 430	19	0.7	60	24	ABN58522	Human spliced tran
C 431	19	0.7	60	24	AAAD29928	Oligonucleotide us
C 432	18.8	0.7	31	22	AAAI30916	Human single nucle
C 433	18.8	0.7	40	22	AAAF75943	TMV-based random 1
C 434	18.8	0.7	40	22	AAAF60055	Oligonucleotide #1
C 435	18.8	0.7	41	24	ABLA0716	Human myosin heavy
C 436	18.8	0.7	41	24	ABLA0717	Human myosin heavy
C 437	18.8	0.7	41	24	ABA98014	Human superoxide d
C 438	18.8	0.7	41	24	ABA95342	Human endoprotease
C 439	18.8	0.7	47	21	AAZ65903	Human map-related
C 440	18.8	0.7	47	21	AAZ66003	Human map-related
C 441	18.8	0.7	47	21	AAZ66884	Human map-related
C 442	18.8	0.7	47	21	AAZ68911	Human map-related
C 443	18.8	0.7	49	13	AAO35798	H6 promoter/HN gen
C 444	18.8	0.7	49	20	AAAV5035	Human E124 PCR 3r1
C 445	18.8	0.7	50	22	AAAL7942	Human SNP oligonuc
C 446	18.8	0.7	50	22	AAAL30708	Human SNP oligonuc
C 447	18.8	0.7	50	22	AAAT78135	Human silent SNP c

448	18.8	0.7	50	22	AAAD03092	1467-04 oligonucle
449	18.8	0.7	50	24	ABL59727	Mycobacterium tube
C 450	18.8	0.7	51	22	AAAL29922	Human SNP oligonuc
C 451	18.8	0.7	51	22	AAAD17720	V. parahaemolyticu
C 452	18.8	0.7	51	22	AAAT74658	Human silent SNP c
C 453	18.8	0.7	51	22	AAAT75286	Human silent SNP c
C 454	18.8	0.7	51	22	AAAT76527	Human silent SNP c
C 455	18.8	0.7	51	22	AAAT76883	Human silent SNP c
C 456	18.8	0.7	51	22	AAAH9547	Human coding sequ
C 457	18.8	0.7	51	22	AAAH9930	Human DNA containi
C 458	18.8	0.7	53	19	AAV04151	PCR product used 1
C 459	18.8	0.7	54	22	AAAS04528	Gene expression pr
C 460	18.8	0.7	56	22	AAAF29832	Library component
C 461	18.8	0.7	57	21	AAAO5800	p12 library varian
C 462	18.8	0.7	58	21	AAAC11140	Human secreted pro
C 463	18.8	0.7	59	22	AAAD6903	Human Oligo 11 to
C 464	18.8	0.7	59	24	ABQ73670	Murine FST1 antise
C 465	18.8	0.7	60	21	AAAC55888	Eucalyptus grandis
C 466	18.8	0.7	60	24	ABN32924	Human spliced tran
C 467	18.8	0.7	60	24	ABN33211	Human spliced tran
C 468	18.8	0.7	60	24	ABN33872	Human spliced tran
C 469	18.8	0.7	60	24	ABN34550	Human spliced tran
C 470	18.8	0.7	60	24	ABN35020	Human spliced tran
C 471	18.8	0.7	60	24	ABN35624	Human spliced tran
C 472	18.8	0.7	60	24	ABN35870	Human spliced tran
C 473	18.8	0.7	60	24	ABN36616	Human spliced tran
C 474	18.8	0.7	60	24	ABN36882	Human spliced tran
C 475	18.8	0.7	60	24	ABN37407	Human spliced tran
C 476	18.8	0.7	60	24	ABN37451	Human spliced tran
C 477	18.8	0.7	60	24	ABN38146	Human spliced tran
C 478	18.8	0.7	60	24	ABN38623	Human spliced tran
C 479	18.8	0.7	60	24	ABN38895	Human spliced tran
C 480	18.8	0.7	60	24	ABN38931	Human spliced tran
C 481	18.8	0.7	60	24	ABN40848	Human spliced tran
C 482	18.8	0.7	60	24	ABN41311	Human spliced tran
C 483	18.8	0.7	60	24	ABN41595	Human spliced tran
C 484	18.8	0.7	60	24	ABN42970	Human spliced tran
C 485	18.8	0.7	60	24	ABN44311	Human spliced tran
C 486	18.8	0.7	60	24	ABN44616	Human spliced tran
C 487	18.8	0.7	60	24	ABN45168	Human spliced tran
C 488	18.8	0.7	60	24	ABN48830	Human spliced tran
C 489	18.6	0.7	25	21	AAAI2188	Human MTF DNA pri
C 490	18.6	0.7	25	24	ABN14634	Human GMLP-1 25-m
C 491	18.6	0.7	27	21	AAAZ51744	N-terminal primer
C 492	18.6	0.7	36	16	AAAT55895	Human TNF-alpha ha
C 493	18.6	0.7	38	21	AAZ47336	PCR primer sexole
C 494	18.6	0.7	39	19	AAV29416	Calcium ion channe
C 495	18.6	0.7	42	18	AAV04442	Antisense primer f
C 496	18.6	0.7	43	21	AAZ45516	Primer Barnaseh102
C 497	18.6	0.7	45	12	AAO12264	Probe to mislasetl
C 498	18.6	0.7	45	24	ABA04690	Peptide B2.7 codin
C 499	18.6	0.7	46	20	AAAI9349	Oligonucleotide LA
500	18.6	0.7	47	15	AAO68630	A33 heavy chain va

ALIGNMENTS

RESULT 1
ID ABN34034 standard; DNA; 60 BP.
AC ABN34034;
XX
DF 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:6782.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
XX splice variant; transcriptome; oligonucleotide library; ss.
OS Homo sapiens.
XX

XX WO020210449-A2.
PD
XX 07-FEB-2002.
PF 20-JUL-2001; 2001WO-IBO1903.
XX
PR 28-JUL-2000; 2000US-221607P.
XX 02-MAY-2001; 2001US-287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A., Wasserman A., Mintz E., Mintz L., Falgler S;
DR WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and developmental-specific genes -
PS Example 1; SEQ ID 6782; 47pp; English.

The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. CC The oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or quantitatively characterizing the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised mini libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue- and pathology-specific genes such as those genes only expressed in specific tissue under a specific pathological condition, to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABNS9589 represent oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention. CC N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. CC

Sequence 60 BP; 16 A; 15 C; 18 G; 11 T; 0 other;

Query Match 2.2%; Score 60; DB 24; Length 60;
Best Local Similarity 100.0%; Pred. NO. 1, de-08;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GQ 1792 GCAGAAGTTTGGCGACGACTTAACCCTGTTAGGCACAAGGGCACAATCAAGTGCCCT 1855
Db 1 GCAAAGATTTCGCCAAGAGCTTAACCTTTAGGCACAAAGAGGCCAACCTCAGTGCCCT 60

RESULT 2
ABL00474/C
ID ABL00474 standard; DNA; 51 BP.
XX
XX ABL00474:
AC
XX
DT 05-MAR-2002 (first entry)
DE
XX Human silent noncoding SNP oligonucleotide SEQ ID NO:465.
KW Human; single nucleotide polymorphism; SNP; polymorphism; cytosolic; immunosuppressive; antiinflammatory; neuroprotective; antimicrobial; autoimmune disease; inflammation; cancer; nervous system disease; infection; polymorphic protein; ds.

[illegible]

XX 24-NOV-1999; 990S-0167383.
 PR (CURA-) CURAGEN CORP.
 PA
 XX
 PI Shinkets RA, Leach M;
 XX
 DR WPI: 2001-355949/37.
 XX
 PT Isolated human nucleic acids comprising one or more single nucleotide
 PT polymorphisms, useful for treating a subject suffering from a
 PT pathology, e.g. autoimmune diseases, ascribed to the presence of a
 PT sequence polymorphism -
 XX
 PS Claim 1; Page 509; 674pp; English.
 PS
 XX ABL00010 to ABL01104 represent human nucleic acid oligonucleotides
 CC comprising one or more single nucleotide polymorphisms (SNPs). ABB56531
 CC to ABB56903 represent human peptides encoded by some of the SNP
 CC oligonucleotides. The sequences from the present invention can have
 CC immunosuppressive, cytostatic, antiinflammatory, neuroprotective and
 CC antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides
 CC and antibodies from the present invention can be used for treating a
 CC subject suffering from, at risk for, or suspected of, suffering from a
 CC pathology ascribed to the presence of a sequence polymorphism. The
 CC pathology may be autoimmune diseases, inflammation, cancer, diseases of
 CC the nervous system, and infection by pathogenic microorganisms. The SNPs
 CC are also useful for determining which forms of a characterised
 CC polymorphism are present in individuals. The antibodies may be used in
 CC the detection, quantitation and/or cellular or tissue localisation of a
 CC polymorphic protein (e.g., for use in measuring levels of the
 CC polymorphic protein within appropriate physiological samples).
 CC
 SQ Sequence 51 BP; 10 A; 14 C; 12 G; 15 T; 0 other;
 SQ
 Query Match 1.8%; Score 49.4; DB 23; Length 51;
 Best Local Similarity 98.0%; Pred. No. 2.8e-05;
 Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1362 AGGAGGTGTGAGCAAGGCTTATGACGAGTACACCTCATCAGACACTTAA 1412
 ID 51 AGGAGGTGTGAGCAAGGCTTATGACGAGTACACCTCATCAGACACTTAA 1
 Db
 RESULT 4
 ABB33915
 ID ABB33915 standard; DNA; 60 BP.
 AC ABB33915;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE Human spliced transcript detection oligonucleotide SEQ ID NO:6663.
 XX
 KM Human; mouse; rat; splice transcript; detection; RNA transcript;
 KM splice variant; transcriptome; oligonucleotide library; ss.
 OS Homo sapiens.
 OS
 XX WO200210449-A2.
 XX
 PD 07-FEB-2002.
 XX
 PF 20-JUL-2001; 2001WO-IB01903.
 XX
 PR 28-JUL-2000; 2000US-221607P.
 PR 02-MAY-2001; 2001US-287724P.
 XX
 PA (COMP-) COMPUGEN INC.
 XX
 PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
 XX
 DR WPI: 2002-257383/30.

XX New oligonucleotide libraries comprising oligonucleotides which
 PT selectively hybridize to mRNAs transcribed from a transcription unit of
 PT a genome, useful for detecting tissue-, pathology-, and
 PT developmental-specific genes -
 XX
 XX Example 1; SEQ ID 6663; 47pp; English.
 XX
 CC The present invention describes oligonucleotide libraries for detecting
 CC messenger RNAs that populate a (sub-)transcriptome, where the
 CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
 CC transcription units that populate a genome. The library comprises
 CC several oligonucleotides, each capable of hybridising selectively to a
 CC set of messenger RNAs transcribed from a given transcription unit of
 CC the genome, which encodes one or more messenger RNA splice variants.
 CC The oligonucleotide libraries are useful for detecting mRNAs from a
 CC biological sample, in expression profiling studies, in qualitatively or
 CC quantitatively characterising the corresponding transcriptome, and in
 CC detecting RNA transcripts and splice variants of human or animal
 CC transcriptomes. The libraries may also be used as specialised mini
 CC libraries to detect transcripts of a sub-transcriptome under a
 CC particular biological or pathological state, and so allowing the
 CC detection of tissue- and pathology-specific genes such as those genes
 CC only expressed in specific tissue under a specific pathological
 CC condition; to detect developmental specific genes; and to detect RNA
 CC transcripts and splice variants of a transcriptome of a patient suffering
 CC from a particular disorder. ABB27253 to ABB59589 represent
 CC oligonucleotide sequences from rats, humans and mice, which are used in
 CC the exemplification of the present invention.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 SQ Sequence 60 BP; 20 A; 19 C; 12 G; 9 T; 0 other;
 SQ
 Query Match 1.3%; Score 35; DB 24; Length 60;
 Best Local Similarity 74.6%; Pred. No. 1.1;
 Matches 44; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
 QY 1041 GCGTTTCGCGAGTCAACCTGATCAGACAGGAGGAGGAGGAGAAAC 1099
 ID 1 GCGTTTCGCGAGTCAACCTGATCAGAGTACAGAGAGGAGGAGGAGAAAC 59
 Db
 RESULT 5
 AA177643
 ID AA177643 standard; DNA; 51 BP.
 AC AA177643;
 XX
 DT 09-NOV-2001 (first entry)
 XX
 DE Human silent SNP containing nucleic acid SEQ:4584.
 XX
 KM Human; single nucleotide polymorphism; SNP; genome; gene therapy;
 KM protein therapy; vaccine; probe; diagnostic assay; detection;
 KM quantitation; restorative therapy; polymorphic; ds.
 OS Homo sapiens.
 OS
 XX WO200140521-A2.
 XX
 PD 07-JUN-2001.
 XX
 PF 30-NOV-2000; 2000WO-US32758.
 XX
 PR 30-NOV-1999; 990S-0168138.
 PR 29-NOV-2000; 2000US-0726173.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shinkets RA, Leach M;
 XX

DR WPI: 2001-356160/37.
XX
PT Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy -
XX
PS Claim 1; Page 1913; 2653pp; English.
XX
CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AAM53114 to AAM53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides.
CC For example, (I) may be used to treat disorders by rectifying mutations
CC or deletions in a patient's genome that affect the activity of
CC polypeptides by expressing inactive proteins or to supplement the
CC patient's own production of polypeptide. Additionally, (I) and its
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar nucleic acids
CC in samples, and therefore which patients may be in need of restorative
CC therapy. The polypeptides encoded by (I) may be used as antigens in the
CC production of antibodies specific for polymorphic polypeptides. The
CC antibodies may also be used to down regulate expression and activity.
CC The antibodies may also be used as diagnostic agents for detecting the
CC presence of polymorphic polypeptides in samples.
XX
SQ Sequence 51 BP; 17 A; 14 C; 13 G; 7 T; 0 other;
XX
Query Match 1.2%; Score 34.6; DB 22; Length 51;
Best Local Similarity 81.6%; Pred. No. 1.4;
Matches 40; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
OY 2375 AGTCAATGCCAGGAGATAGGGGTGGTACCTGTTGAAACCCCACT 2423
ID 1 AGACAAATGCTTAGGACGATAGGGGTAGGTCACAGTGAACCCCACT 49
Db
RESULT 6
ID AA126919 standard; DNA: 51 BP.
XX
AC AA126919;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #127.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PE 28-DEC-2000; 2000WO-US35498.
XX
PR 28-DEC-1999; 99US-0173419.
XX
PT 27-DEC-2000; 2000US-0173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI: 2001-465210/50.

XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections -
XX
PS Claim 1; Page 1434; 4143pp; English.
XX
CC The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC G-protein coupled receptors and thioesterases. The present sequence is
CC one such oligonucleotide. The oligonucleotides and the peptides encoded
CC by them may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate expression of the proteins listed
CC above. Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (leukaemia), diseases of the bladder, brain, breast, colon and kidney,
CC organisms.
XX
SQ Sequence 51 BP; 19 A; 11 C; 10 G; 11 T; 0 other;
XX
Query Match 1.2%; Score 33.6; DB 22; Length 51;
Best Local Similarity 81.2%; Pred. No. 2.8;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
OY 1057 CAACCTGATTCACATCAGAGACACCTCAGGGGAGAAACCTTATG 1104
ID 1 CAACCTGATTTGATCATCAGAGAACATCATCAGAGAGAAACCTATG 48
Db
RESULT 7
ID AA177642
XX
AC AA177642;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:4583.
XX
KW Human: single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX
OS Homo sapiens.
XX
PN WO200140521-A2.
XX
PD 07-JUN-2001.
XX
PE 30-NOV-2000; 2000WO-US32758.
XX
PR 30-NOV-1999; 99US-0168138.
XX
PT 29-NOV-2000; 2000US-0726173.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI: 2001-356160/37.
XX
PT Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy -
XX
PS Claim 1; Page 1913; 2653pp; English.
XX
CC AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

CC detecting RNA transcripts and splice variants of human or animal
CC transcripts. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX
SQ Sequence 60 BP; 19 A; 11 C; 20 G; 10 T; 0 other;

Query Match 1.1%; Score 31; DB 24; Length 60;
Best Local Similarity 87.2%; Pred. No. 21;
Matches 34; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1419 CACACAGAGAGAGCCTTATGTATGCACAGATGTGGG 1457
|||||
DB 15 CACACAGAGAGAGAGCCTTATGTATGCACAGATGTGGG 53

RESULT 10
ABN34117
ID ABN34117 standard; DNA; 60 BP.
XX
AC ABN34117;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:6865.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KM splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-1B01903.
XX
PR 28-JUL-2000; 2000US-221607P.
XX
PR 02-MAY-2001; 2001US-287724P.
XX
PA (COMP-) COMPUEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
DR WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes
XX
XX
PS Example 1; SEQ ID 6865; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridising selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in

CC detecting RNA transcripts and splice variants of human or animal
CC transcripts. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX
SQ Sequence 60 BP; 16 A; 12 C; 16 G; 16 T; 0 other;

Query Match 1.1%; Score 30.6; DB 24; Length 60;
Best Local Similarity 73.6%; Pred. No. 28;
Matches 39; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 1849 CCTTGTGTGAGGAGGTGGCGAAGCCTTTGTGCTAAGTAACTCATTT 1901
|||||
DB 6 CCTTGTGTGCAAGAGGTGTGCAAGCCTTTGTGAGTATAGGCCAGTTTCATT 58

RESULT 11
ABN34244
ID ABN34244 standard; DNA; 60 BP.
XX
AC ABN34244;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:6992.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KM splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-1B01903.
XX
PR 28-JUL-2000; 2000US-221607P.
XX
PR 02-MAY-2001; 2001US-287724P.
XX
PA (COMP-) COMPUEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
DR WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes
XX
XX
PS Example 1; SEQ ID 6992; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridising selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterising the corresponding transcriptome, and in

CC detecting RNA transcripts and splice variants of human or animal
CC transcripts. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX

SO Sequence 60 BP; 18 A; 15 C; 15 G; 12 T; 0 other;

Query Match 1.0%; Score 28.6; DB 24; Length 60;
Best Local Similarity 67.8%; Pred. No. 1.2e+02;
Matches 40; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 1302 CAGGATTCACACCGTCGACAGACACATCATCAGAGAGAGCCCTTCATTG 1360
DB 1 CAGAGTTCTAACGTGGTGTCTATCACAAGACATGCCAGAGAGCCCTTACAGTGG 59

RESULT 14
AA179453
ID AA179453 standard; DNA: 51 BP.
AC AA179453:
DT 09-NOV-2001 (first entry)
XX

DE Human silent SNP containing nucleic acid SEQ:6394.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX
OS Homo sapiens.
XX
PN WO200140521-A2.
XX
PD 07-JUN-2001.
XX
PE 30-NOV-2000; 2000WO-US32758.
XX
PR 30-NOV-1999; 99US-0168138.
PR 29-NOV-2000; 2000US-0726173.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2001-356160/37.
XX
PT Polymorphic nucleic acid sequences, useful in genetic testing and
XX therapy -
XX
PS Claim 1; Page 2464; 2653bp; English.
XX

AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA153114 to AA153329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides.
CC For example, (I) may be used to treat disorders by rectifying mutations
CC or deletions in a patient's genome that affect the activity of
CC polypeptides by expressing inactive proteins or to supplement the
CC patients own production of polypeptide. Additionally, (I) and its

CC complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar nucleic acids
CC in samples, and therefore which patients may be in need of restorative
CC therapy. The polypeptides encoded by (I) may be used as antigens in the
CC production of antibodies specific for polymorphic polypeptides. The
CC antibodies may also be used to down regulate expression and activity.
CC The antibodies may also be used as diagnostic agents for detecting the
CC presence of polymorphic polypeptides in samples.
XX

SO Sequence 51 BP; 16 A; 6 C; 18 G; 11 T; 0 other;

Query Match 1.0%; Score 27.8; DB 22; Length 51;
Best Local Similarity 74.5%; Pred. No. 1.9e+02;
Matches 35; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1243 AGAGGGCGCACACTGGGAGAGAGCCTTATGTTCCAGAGATGCGG 1289
DB 1 AGAGAGTCACACTGAGAGAAACCTTATGATGTGTGATGCGG 47

RESULT 15
AA178093/C
ID AA178093 standard; DNA: 51 BP.
AC AA178093:
DT 09-NOV-2001 (first entry)
XX
XX
DE Human silent SNP containing nucleic acid SEQ:5034.
XX
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX
OS Homo sapiens.
XX
PN WO200140521-A2.
XX
PD 07-JUN-2001.
XX
PE 30-NOV-2000; 2000WO-US32758.
XX
PR 30-NOV-1999; 99US-0168138.
PR 29-NOV-2000; 2000US-0726173.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2001-356160/37.
XX
PT Polymorphic nucleic acid sequences, useful in genetic testing and
XX therapy -
XX
PS Claim 1; Page 2050; 2653bp; English.
XX

AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA153114 to AA153329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides.
CC For example, (I) may be used to treat disorders by rectifying mutations
CC or deletions in a patient's genome that affect the activity of
CC polypeptides by expressing inactive proteins or to supplement the
CC patients own production of polypeptide. Additionally, (I) and its
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar nucleic acids
CC in samples, and therefore which patients may be in need of restorative
CC therapy. The polypeptides encoded by (I) may be used as antigens in the
CC production of antibodies specific for polymorphic polypeptides. The
CC antibodies may also be used to down regulate expression and activity.

RESULT 18
AAL33199
ID AAL33199 standard; DNA; 51 BP


```

XX AC AAL33199;
XX XX
XX 24-JAN-2002 (first entry)
XX DE Human SNP oligonucleotide #6407.
XX XX
XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
XX neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
XX amyloid protein; angiotensin; apoptosis related protein; cadherin;
XX cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
XX complement related protein; cytochrome; kinesin; cytokine; interferon;
XX interleukin; G-protein coupled receptor; thioesterase; inflammation;
XX multifactorial disease; autoimmune disease; infection;
XX nervous system disease; ss.
XX OS Homo sapiens.
XX PN WO200147944-A2.
XX XX
XX 05-JUL-2001.
XX PD
XX PF 28-DEC-2000; 2000WO-US35498.
XX PR 28-DEC-1999; 99US-0173419.
XX PR 27-DEC-2000; 2000US-0173419.
XX XX
XX PA (CURA-) CURAGEN CORP.
XX PI Shinkets RA, Leach M;
XX DR WPI; 2001-465210/50.
XX XX
XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX PT oncogenes and histones, useful for diagnosing and treating, e.g.
XX cancer, autoimmune diseases and infections.
XX PS
XX Claim 1; Page 3217; 4143pp; English.
XX CC
XX The present invention relates to oligonucleotides encoding polymorphic
XX variants of proteins related to amylases, amyloid proteins, angiotensin,
XX apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
XX histones, kinases, colony stimulating factors, complement related
XX proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
XX G-protein coupled receptors and thioesterases. The present sequence is
XX one such oligonucleotide. The oligonucleotides and the peptides encoded
XX by them may be used in the prevention, diagnosis and treatment of
XX diseases associated with inappropriate expression of the proteins listed
XX above. Disorders that may be prevented, diagnosed and/or treated include
XX multifactorial diseases with a genetic component, such as autoimmune
XX diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
XX systemic lupus erythematosus and Grave's disease), inflammation, cancer
XX (e.g. cancers of the bladder, brain, breast, colon and kidney,
XX leukaemia), diseases of the nervous system and an infection of pathogenic
XX organisms.
XX CC
XX
XX Sequence 51 BP; 19 A; 17 C; 11 G; 4 T; 0 other;
SQ
Query Match 1.0%; Score 26.8; DB 22; Length 51;
Best Local Similarity 73.9%; Pred. No. 4e+02;
Matches 34; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
OY 1560 TCAACCTTACAGACACAGAGCGGAGGAGGCAT 1605
DB 1 TCAACCTGACATCCACACAGACACAGAGAGAGGCCCT 46

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DT 30-JUL-2002 (first entry)
XX XX
XX Probe #2 for kruppel zinc finger related protein 70.84 CDNA.
XX DE
XX XX
XX Human; kruppel zinc finger related protein 70.84; tumour;
XX KW haemal disorder; HIV infection; immunological disease; inflammation;
XX KW gene therapy; probe; ss.
XX OS Homo sapiens.
XX PN WO200226807-A1.
XX PD
XX 04-APR-2002.
XX PF
XX 02-JUL-2001; 2001WO-CN01114.
XX PR
XX 07-JUL-2000; 2000CN-0117012.
XX XX
XX (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX PA
XX PI Mao Y, Xie Y;
XX DR WPI; 2002-292482/33.
XX XX
XX Human Kruppel zinc finger related protein 70.84 and encoding
XX PT polynucleotide, useful in the diagnosis and treatment of malignant
XX PT tumours, haemal disorders, human immunodeficiency virus infection,
XX PT immunological diseases and inflammation.
XX XX
XX Example 7; Page 15; 39pp; Chinese.
XX PS
XX Probes ABL56733-34 were used to identify cDNA encoding a human
XX CC kruppel zinc finger related protein 70.84. The polypeptide and its
XX CC encoding polynucleotide are used in diagnosis and treatment of
XX CC malignant tumour, haemal disorders, human immunodeficiency virus (HIV)
XX CC infection, immunological diseases and various inflammations. The
XX CC polynucleotide may also be used for gene therapy.
XX XX
XX Sequence 41 BP; 8 A; 9 C; 12 G; 12 T; 0 other;
SQ
Query Match 1.0%; Score 26.6; DB 24; Length 41;
Best Local Similarity 78.0%; Pred. No. 4e+02;
Matches 32; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
OY 301 TGCAGACCTATACCATCTGCGTCACGGAATTCGA 341
DB 1 TGCAGACATTTATGGGAATCTGGCTCTCCGCAATTCCA 41

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RESULT 20
AAS18906
ID AAS18906 standard; DNA; 41 BP.
XX AC AAS18906;
XX XX
XX 26-MAR-2002 (first entry)
XX DE
XX XX
XX Human OZF gene related protein 13 oligonucleotide probe #1.
XX DE
XX XX
XX Human; ss; OZF gene related protein 13; cancer; HIV infection;
XX KW human immunodeficiency virus; probe.
XX KW
XX OS Homo sapiens.
XX PN CN131534-A.
XX XX
XX 03-OCT-2001.
XX PD
XX 27-MAR-2000; 2000CN-0115166.
XX PF
XX 27-MAR-2000; 2000CN-0115166.
XX PR
XX PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.

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XX  Mao Y, Xie Y;
XX  WPI: 2002-056303/08.
XX  PolyPeptide-OZF gene related protein 13 and polynucleotide encoding
XX  it
XX  Example 7; Page 20; 31pp; Chinese.
XX
XX  The invention relates to a new polypeptide-OZF (not defined) gene related
XX  protein 13, the polynucleotide encoding it, the process for preparing the
XX  said polypeptide by DNA recombination, the application of said
XX  polypeptide in treating several diseases such as cancer and HIV infection
XX  (human immunodeficiency virus). The antagonist against the said
XX  polypeptide and its therapeutic action, and the application of said
XX  polynucleotide for coding this new-OZF correlated protein 13 are
XX  disclosed. The present sequence is an oligonucleotide probe used to
XX  detect nucleic acids encoding OZF gene related protein 13.
XX
XX  Sequence 41 BP; 15 A; 6 C; 11 G; 9 T; 0 other;
XX
XX  Query Match      1.0%; Score 26.6; DB 24; Length 41;
XX  Best Local Similarity 78.0%; Pred. No. 4e+02;
XX  Matches 32; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
XX
XX  1411 TAAGACACACACAGAGAGAGCCTTATGTATGCACAGAA 1451
XX  1 TCGAAGTCACACAGCTGAGAGCCCTTATGTATGTATGAA 41
XX
XX  RESULT 21
XX  AAH89605/C
XX  ID AAH89605 standard; DNA; 51 BP.
XX
XX  AAH89605;
XX
XX  01-OCT-2001 (first entry)
XX
XX  Human DNA/RNA binding protein DNA polymorphic site SEQ ID NO: 386.
XX
XX  Human; single nucleotide polymorphism; SNP; paternity test;
XX  forensic test; aberrant protein expression; ds.
XX
XX  Homo sapiens.
XX
XX  WO200151670-A2.
XX
XX  19-JUL-2001.
XX
XX  05-JAN-2001; 2001WO-US00322.
XX
XX  07-JAN-2000; 2000US-0174962.
XX
XX  (CURA-) CURAGEN CORP.
XX
XX  Shimkets RA, Leach MD;
XX  WPI: 2001-451871/48.
XX  P-PSDB; AAM00488.
XX
XX  Isolated human polynucleotides containing single nucleotide
XX  polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
XX  infection and diabetes -
XX
XX  Claim 1; Page 213; 475pp; English.
XX
XX  The present invention relates to human nucleic acids containing single
XX  nucleotide polymorphisms (SNPs). These can be used in forensic and
XX  paternity tests, and to aid in the treatment of diseases associated with
XX  aberrant protein expression, including cancer, amyloidosis, diabetes,
XX  Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
XX  glomerulonephritis, haemolytic anaemia, thrombocytopenia, arthritis,

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CC  meningitis, muscular disorders, dementia, neurological diseases, tubercous
CC  sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
CC  osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
CC  autoimmunity. The present sequence is a polymorphism-containing
CC  oligonucleotide fragment of the invention.
XX
XX  Sequence 51 BP; 6 A; 13 C; 23 G; 9 T; 0 other;
XX
XX  Query Match      1.0%; Score 26.6; DB 22; Length 51;
XX  Best Local Similarity 71.4%; Pred. No. 4.6e+02;
XX  Matches 35; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
XX
XX  1960 GCTTAGCCGCGCATGCACACCTCATTTAGACACAGACATTCAGG 2008
XX  49 GCTTCAGCGCGCCCTTCGACACCTGCGTCCGCCACACGAGACTACACAGG 1
XX
XX  RESULT 22
XX  AAD33627
XX  ID AAD33627 standard; DNA; 56 BP.
XX
XX  AAD33627;
XX
XX  01-JUL-2002 (first entry)
XX
XX  21f-3 specific sense oligo used to generate three finger ZFP.
XX
XX  DNA binding protein; zinc finger domain 3; zinc finger protein; ZFP;
XX  viral replication; gene expression; virucide; Zif3; ss.
XX
XX  Unidentified.
XX
XX  WO200208286-A2.
XX
XX  31-JAN-2002.
XX
XX  19-JUL-2001; 2001WO-EP08367.
XX
XX  21-JUL-2000; 2000US-220060P.
XX
XX  (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
XX  Sera T;
XX
XX  WPI: 2002-172000/22.
XX
XX  Example 7; Page 72; 143pp; English.
XX
XX  The present invention relates to novel DNA binding proteins comprising
XX  zinc finger domains in which two histidine and two cysteine residues
XX  coordinate a central zinc ion. The invention particularly relates to
XX  the identification of a context-independent recognition code to design
XX  zinc finger domains. The invention also relates to zinc finger proteins
XX  (ZFP) designed using this recognition code. The ZFPs are useful for
XX  altering genomic structure, inhibiting viral replication (where viral
XX  replication is inhibited for plant virus, an animal virus or a human
XX  virus), modulating gene expression, detecting an altered zinc finger
XX  recognition sequence and diagnosing disease associated with abnormal
XX  genomic structure. The present DNA sequence is zinc finger domain 3
XX  (Zif-3) specific oligonucleotide which is used to generate three finger
XX  ZFP for the 11 site of beet curly top virus (BCTV). This sequence is
XX  used in the exemplification of the invention.
XX
XX  Sequence 56 BP; 15 A; 10 C; 19 G; 12 T; 0 other;
XX
XX  Query Match      1.0%; Score 26.6; DB 24; Length 56;
XX  Best Local Similarity 71.4%; Pred. No. 4.9e+02;
XX  Matches 35; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
XX
XX  921 GGGGAGACACCTTATCATGTACTGAGTGGGAGACAGCTTGGCAGTA 969

```


DE zif-1 specific sense oligo used to generate three finger ZFP.
 XX
 KW DNA binding protein; zinc finger domain 1; zinc finger protein; ZFP;
 XX viral replication; gene expression; virucide; zif1; ss.
 XX
 OS Unidentified.
 XX
 PN WO200208286-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 19-JUL-2001; 2001WO-EP08367.
 XX
 PR 21-JUL-2000; 2000US-220060P.
 XX
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 PI Sera T;
 XX
 DR WPI: 2002-172000/22.
 XX
 PT New Zinc Finger Protein (ZFP) comprising three essential domains useful
 XX for diagnosing diseases associated with abnormal genomic structure -
 XX
 PS Example 7; Page 71; 143pp; English.
 XX
 CC The present invention relates to novel DNA binding proteins comprising
 CC zinc finger domains in which two histidine and two cysteine residues
 CC coordinate a central zinc ion. The invention particularly relates to
 CC the identification of a context-independent recognition code to design
 CC zinc finger domains. The invention also relates to zinc finger proteins
 CC (ZFP) designed using this recognition code. The ZFPs are useful for
 CC altering genomic structure, inhibiting viral replication (where viral
 CC replication is inhibited for plant virus, an animal virus or a human
 CC virus), modulating gene expression, detecting an altered zinc finger
 CC recognition sequence and diagnosing disease associated with abnormal
 CC genomic structure. The present DNA sequence is zinc finger domain 1
 CC (Zif-1) specific oligonucleotide which is used to generate three finger
 CC ZFP for the LI site of beet curly top virus (BCTV). This sequence is
 CC used in the exemplification of the invention.
 XX
 SQ Sequence 60 BP; 18 A; 9 C; 19 G; 14 T; 0 other;
 XX
 Query Match 0.9%; Score 25.8; DB 24; Length 60;
 Best Local Similarity 73.3%; Pred. No. 9.2e+02;
 Matches 33; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 OY 1593 GGGGAGAACCCATTGTATGTCGAGTCGGGAGCGCTTACC 1637
 DB 1 GGGGAGAACCCGCTATTAATGTCGGAATGTGTAAAGCTTTAGC 45
 XX
 RESULT 26
 AAD33618
 ID AAD33618 standard; DNA: 56 BP.
 AC AAD33618;
 DT 01-JUL-2002 (first entry)
 XX
 DE zif-3 specific PCR primer 5 used to generate three finger ZFP.
 XX
 KW DNA binding protein; zinc finger domain 3; zinc finger protein; ZFP;
 KW viral replication; gene expression; virucide; zif3; PCR; primer; ss.
 XX
 OS Unidentified.
 XX
 PN WO200208286-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 19-JUL-2001; 2001WO-EP08367.
 XX

PR 21-JUL-2000; 2000US-220060P.
 XX
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 PI Sera T;
 XX
 DR WPI: 2002-172000/22.
 XX
 PT New Zinc Finger Protein (ZFP) comprising three essential domains useful
 XX for diagnosing diseases associated with abnormal genomic structure -
 XX
 PS Example 6; Page 71; 143pp; English.
 XX
 CC The present invention relates to novel DNA binding proteins comprising
 CC zinc finger domains in which two histidine and two cysteine residues
 CC coordinate a central zinc ion. The invention particularly relates to
 CC the identification of a context-independent recognition code to design
 CC zinc finger domains. The invention also relates to zinc finger proteins
 CC (ZFP) designed using this recognition code. The ZFPs are useful for
 CC altering genomic structure, inhibiting viral replication (where viral
 CC replication is inhibited for plant virus, an animal virus or a human
 CC virus), modulating gene expression, detecting an altered zinc finger
 CC recognition sequence and diagnosing disease associated with abnormal
 CC genomic structure. The present DNA sequence is zinc finger domain 3
 CC (Zif-3) specific PCR primer 5 used to generate three finger ZFP. This
 CC sequence is used in the exemplification of the invention.
 XX
 SQ Sequence 56 BP; 13 A; 9 C; 16 G; 10 T; 8 other;
 XX
 Query Match 0.9%; Score 25.6; DB 24; Length 56;
 Best Local Similarity 72.1%; Pred. No. 1e+03;
 Matches 31; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 OY 1179 AAGCCTTATGTCGACGATGCGGACGCTTACCTCA 1221
 DB 7 AAGCCTTACAGTGCCTGAATGCGGAAGACTTACTNNNA 49
 XX
 RESULT 27
 ABN34081
 ID ABN34081 standard; DNA: 60 BP.
 AC ABN34081;
 DT 15-JUL-2002 (first entry)
 XX
 DE Human spliced transcript detection oligonucleotide SEQ ID NO:6629.
 XX
 KW Human; mouse; rat; splice transcript; detection; RNA transcript;
 KW splice variant; transcriptome; oligonucleotide library; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200210449-A2.
 XX
 PD 07-FEB-2002.
 XX
 PF 20-JUL-2001; 2001WO-IB01903.
 XX
 PR 28-JUL-2000; 2000US-221607P.
 PR 02-MAY-2001; 2001US-287724P.
 XX
 PA (COMP-) COMPUGEN INC.
 XX
 PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
 XX
 DR WPI: 2002-257383/30.
 XX
 PT New oligonucleotide libraries comprising oligonucleotides which
 PT selectively hybridize to mRNAs transcribed from a transcription unit of
 PT a genome, useful for detecting tissue-, pathology-, and
 PT developmental-specific genes
 XX

PS Example 1; SEQ ID 6829; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridizing selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterizing the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 60 BP; 19 A; 11 C; 10 G; 20 T; 0 other;
XX
Query Match 0.9%; Score 25.6; DB 24; Length 60;
Best Local Similarity 66.1%; Pred. No. 1.1e+03;
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
OY 1190 GTGCAAGAAATGTGGCAGACCTTAGCGTCAAGTCAACCTCATTCACACCGA 1245
DB 4 GTGTGAGAAATGTGGCAAGACCTTATCTGTCTCTCATCTTACACATAGA 59
RESULT 28
ABN34388
ID ABN34388 standard; DNA: 60 BP.
XX
AC ABN34388;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:7136.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PE 20-JUL-2001; 2001WO-IB01903.
XX
PR 28-JUL-2000; 2000US-221607P.
XX
PR 02-MAY-2001; 2001US-287724P.
XX
XX (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
DR WPI: 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes
XX

PS Example 1; SEQ ID 7136; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridizing selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.
CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterizing the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a transcriptome of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 60 BP; 17 A; 13 C; 17 G; 13 T; 0 other;
XX
Query Match 0.9%; Score 25.4; DB 24; Length 60;
Best Local Similarity 68.6%; Pred. No. 1.2e+03;
Matches 35; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
OY 1360 GCAGGAAATGTGGCAGACCTTAGCGTCAAGTCAACCTCATTCAGAACT 1410
DB 8 GTAGCAATGTGGAGCCAGCGCTGTCCAGAGATTCTCATCAGCAGATAGT 58
RESULT 29
ABA03765
ID ABA03765 standard; DNA: 41 BP.
XX
AC ABA03765;
XX
DT 18-FEB-2002 (first entry)
XX
DE Human actin 15 DNA probe 1.
XX
KW Human; zinc finger; PHD finger; actin 15; cancer; nosohaemia;
KW HIV; human immunodeficiency virus; infection; immunological disease;
KW inflammatory disorder; probe; ss.
XX
XX
OS Homo sapiens.
XX
PN CN1307041-A.
XX
PD 08-AUG-2001.
XX
PE 26-JAN-2000; 2000CN-0111549.
XX
PR 26-JAN-2000; 2000CN-0111549.
XX
XX (BODA-) BODAO GENE TECH CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI: 2002-062743/09.
XX
XX
PT Polypeptide-human zinc finger and PHD finger structural domain-contg
PT actin 15 and polynucleotide for coding said polypeptide -
XX
XX Example 7; Page 21 (disclosure); 35pp; Chinese.
XX

CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 60 BP; 17 A; 13 C; 14 G; 16 T; 0 other;

Query Match 0.9%; Score 25.2; DB 24; Length 60;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;

Matches 36; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

OY 1225 CAACGCTTATACCGACGAGGGCGGCGACTGGGGAGACCTTATGTTTCA 1278
DB 5 CACACCTGACTGACATCAGAGGGTTCATCTGAGAGACGACCTTGAATGTA 58

RESULT 32

ABN45438
ID ABN45438 standard; DNA; 60 BP.

AC ABN45438;

DT 15-JUL-2002 (first entry)

DE Human spliced transcript detection oligonucleotide SEQ ID NO:18186.

XX Human; mouse; rat; splice transcript; detection; RNA transcript;

KW splice variant; transcriptome; oligonucleotide library; ss.

XX Homo sapiens.

OS WO200210449-A2.

PN 07-FEB-2002.

PD 20-JUL-2001; 2001WO-1B01903.

PE 28-JUL-2000; 2000US-221607P.

PR 02-MAY-2001; 2001US-287724P.

XX (COMP-) COMPUGEN INC.

PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

DR WPI; 2002-257383/30.

PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes

PS Example 1; SEQ ID 18186; 47pp; English.

XX The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises
CC several oligonucleotides, each capable of hybridizing selectively to a
CC set of messenger RNAs transcribed from a given transcription unit of
CC the genome, which encodes one or more messenger RNA splice variants.

CC The oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterizing the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a
CC particular biological or pathological state, and so allowing the
CC detection of tissue- and pathology-specific genes such as those genes
CC only expressed in specific tissue under a specific pathological
CC condition; to detect developmental specific genes; and to detect RNA
CC transcripts and splice variants of a patient suffering
CC from a particular disorder. ABN27253 to ABN59589 represent
CC oligonucleotide sequences from rats, humans and mice, which are used in
CC the exemplification of the present invention.

CC N.B. The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 60 BP; 19 A; 16 C; 10 G; 15 T; 0 other;

Query Match 0.9%; Score 25.2; DB 24; Length 60;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;

Matches 36; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

OY 1192 GCAAGGATGTGGCAGAGCTTTAGCCTGAAGCTCAACCTATTACCACGAGA 1245
DB 1 GCAATGAACTGGGAGAAACCTTTCATGATGATCCTTCATCCTCATCAGA 54

RESULT 33

ABL56733
ID ABL56733 standard; DNA; 41 BP.

AC ABL56733;

DT 30-JUL-2002 (first entry)

DE Probe #1 for Kruppel zinc finger related protein 70.84 cDNA.

XX Human; Kruppel zinc finger related protein 70.84; tumour;

KW haemal disorder; HIV infection; immunological disease; inflammation;

XX gene therapy; probe; ss.

XX Homo sapiens.

OS WO200226807-A1.

PN 04-APR-2002.

PD 02-JUL-2001; 2001WO-CN01114.

PE 07-JUL-2000; 2000CN-0117012.

XX (BLOW-) BLOWINDOM GENE DEV INC SHANGHAI.

PI Mao Y, Xie Y;

DR WPI; 2002-292482/33.

PT Human Kruppel zinc finger related protein 70.84 and encoding
PT polynucleotide, useful in the diagnosis and treatment of malignant
PT tumours, haemal disorders, human immunodeficiency virus infection,
PT immunological diseases and inflammation

PS Example 7; Page 15; 39pp; Chinese.

XX Probes ABL56733-34 were used to identify cDNA encoding a human
CC Kruppel zinc finger related protein 70.84. The polypeptide and its
CC encoding polynucleotide are used in diagnosis and treatment of
CC malignant tumour, haemal disorders, human immunodeficiency virus (HIV)
CC infection, immunological diseases and various inflammations. The
CC polynucleotide may also be used for gene therapy.

XX Sequence 41 BP; 8 A; 8 C; 13 G; 12 T; 0 other;

Query Match 0.9%; Score 25; DB 24; Length 41;
Best Local Similarity 75.6%; Pred. No. 1.3e+03;

Matches 31; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 301 TGCTGAGACTTATTAACCATCTGCTGCTGAGTAATTCGA 341
DB 1 TGCTGAGAAATTAATGGAATGTGGCTCCCTGGGATTTCGA 41

RESULT 34

AAS18907
ID AAS18907 standard; DNA; 41 BP.

XX

PR 02-MAY-2001; 2001US-287724P.
XX
XX (COMP-) COMPUGEN INC.
PA
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
PI
XX WPI; 2002-257383/30.
DR
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes
PS
PS Example 1; SEQ ID 6664; 47pp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the
XX (sub-)transcriptome comprises messenger RNAs transcribed from multiple
XX transcription units that populate a genome. The library comprises
XX several oligonucleotides, each capable of hybridizing selectively to a
XX set of messenger RNAs transcribed from a given transcription unit of
XX the genome, which encodes one or more messenger RNA splice variants.
XX The oligonucleotide libraries are useful for detecting mRNAs from a
XX biological sample, in expression profiling studies, in qualitatively or
XX quantitatively characterizing the corresponding transcriptome, and in
XX detecting RNA transcripts and splice variants of human or animal
XX transcriptomes. The libraries may also be used as specialised mini
XX libraries to detect transcripts of a sub-transcriptome under a
XX particular biological or pathological state, and so allowing the
XX detection of tissue- and pathology-specific genes such as those genes
XX only expressed in specific tissue under a specific pathological
XX condition; to detect developmental specific genes; and to detect RNA
XX transcripts and splice variants of a transcriptome of a patient suffering
XX from a particular disorder. ABN27253 to ABN59589 represent
XX oligonucleotide sequences from rats, humans and mice, which are used in
XX the exemplification of the present invention.
XX N.B. The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
SQ Sequence 60 BP; 24 A; 8 C; 12 G; 16 T; 0 other;
Query Match 0.9%; Score 24.8; DB 24; Length 60;
Best Local Similarity 63.3%; Pred. No. 1.9e+03;
Matches 38; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
OY 1659 CACGAGGACACACTGAGGAGAGGACATTGTATGTGCTGAGTGAGCAGAGCCTT 1718
DB 1 CATCAGATACCCACTTAGAAGAGAACAAATGTAAATGTGATATATGCGCAAGCTATTT 60
RESULT 37
ABN34111
ID ABN34111 standard; DNA: 60 BP.
XX
XX ABN34111;
AC
XX
XX 15-JUL-2002 (first entry)
DT
XX
XX Human spliced transcript detection oligonucleotide SEQ ID NO:6859.
DE
XX
XX Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200210449-A2.
FN
XX
XX 07-FEB-2002.
PD
XX
XX 20-JUL-2001; 2001WO-IB01903.
PE
XX
XX 28-JUL-2000; 2000US-221607P.
PR

PR 02-MAY-2001; 2001US-287724P.
XX
XX (COMP-) COMPUGEN INC.
PA
XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
PI
XX WPI; 2002-257383/30.
DR
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of
PT a genome, useful for detecting tissue-, pathology-, and
PT developmental-specific genes
PS
PS Example 1; SEQ ID 6859; 47pp; English.
XX
XX The present invention describes oligonucleotide libraries for detecting
XX messenger RNAs that populate a (sub-)transcriptome, where the
XX (sub-)transcriptome comprises messenger RNAs transcribed from multiple
XX transcription units that populate a genome. The library comprises
XX several oligonucleotides, each capable of hybridizing selectively to a
XX set of messenger RNAs transcribed from a given transcription unit of
XX the genome, which encodes one or more messenger RNA splice variants.
XX The oligonucleotide libraries are useful for detecting mRNAs from a
XX biological sample, in expression profiling studies, in qualitatively or
XX quantitatively characterizing the corresponding transcriptome, and in
XX detecting RNA transcripts and splice variants of human or animal
XX transcriptomes. The libraries may also be used as specialised mini
XX libraries to detect transcripts of a sub-transcriptome under a
XX particular biological or pathological state, and so allowing the
XX detection of tissue- and pathology-specific genes such as those genes
XX only expressed in specific tissue under a specific pathological
XX condition; to detect developmental specific genes; and to detect RNA
XX transcripts and splice variants of a transcriptome of a patient suffering
XX from a particular disorder. ABN27253 to ABN59589 represent
XX oligonucleotide sequences from rats, humans and mice, which are used in
XX the exemplification of the present invention.
XX N.B. The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
SQ Sequence 60 BP; 13 A; 14 C; 18 G; 15 T; 0 other;
Query Match 0.9%; Score 24.8; DB 24; Length 60;
Best Local Similarity 67.3%; Pred. No. 1.9e+03;
Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
OY 204 GAGCGCTTCGCGCATTCAGGAGATGCTGTGACTTCACCCAGAGAGACT 255
DB 9 GAGCAATTGTGACCCCTCAAGAGATGCGCATGACCTTCACCTTGGAGACT 60
RESULT 38
ABA03751
ID ABA03751 standard; DNA: 41 BP.
XX
XX ABA03751;
AC
XX
XX 18-FEB-2002 (first entry)
DT
XX
XX Human zinc finger protein 22 DNA probe 1.
DE
XX
XX Human; zinc finger protein 22; cancer; nosohaemia; infection;
KW HIV; human immunodeficiency virus; immunological disease;
KW inflammatory disorder; probe; ss.
XX
XX Homo sapiens.
OS
XX
XX CN1307039-A.
FN
XX
XX 08-AUG-2001.
PD
XX
XX 26-JAN-2000; 2000CN-0111545.
PE
XX
XX

PR 26-JAN-2000; 2000CN-0111545.
XX
XX (BODA-) BODAO GENE TECH CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-062741/09.
XX
PT Polypeptide-human zinc finger protein 22 and polynucleotide for coding
XX said polypeptide -
XX
PS Example 7; Page 20 (disclosure); 34pp; Chinese.
XX
CC The invention relates to a novel polypeptide, human zinc finger protein
CC 22. The polypeptide is useful for treating various diseases, such as
CC malignant tumours, nosohaemia, HIV infection, immunological diseases and
CC inflammatory disorder. The present sequence is a probe used to
CC detect polynucleotides encoding the polypeptide of the invention.
XX
SQ Sequence 41 BP; 17 A; 8 C; 11 G; 5 T; 0 other; .

Query Match 0.9%; Score 24.6; DB 24; Length 41;
Best Local Similarity 76.9%; Pred. No. 1.7e+03;
Matches 30; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1066 TCACACATCAGAGGACACACCTCAGGGAACCTTATG 1104
DB 1 TGAGACATCAGAGAGTGCACACAGAGAGAAACCTTACG 39

RESULT 39
ABA03752
ID ABA03752 standard; DNA: 41 BP.
AC ABA03752;
XX
XX 18-FEB-2002 (first entry)
DT
XX
DE Human zinc finger protein 22 DNA probe 2.
XX
XX Human; zinc finger protein 22; cancer; nosohaemia; infection;
KW HIV; human immunodeficiency virus; immunological disease;
XX
XX Inflammatory disorder; probe; ss.
OS
XX Homo sapiens.
OS
XX
XX CN1307039-A.
XX
XX 08-AUG-2001.
PD
XX
XX 26-JAN-2000; 2000CN-0111545.
PF
XX
XX 26-JAN-2000; 2000CN-0111545.
PR
XX
XX (BODA-) BODAO GENE TECH CO LTD SHANGHAI.
PA
XX
XX Mao Y, Xie Y;
PI
XX
XX WPI; 2002-062741/09.
DR
XX
XX Polypeptide-human zinc finger protein 22 and polynucleotide for coding
PT said polypeptide -
XX
XX
PS Example 7; Page 20 (disclosure); 34pp; Chinese.
XX
CC The invention relates to a novel polypeptide, human zinc finger protein
CC 22. The polypeptide is useful for treating various diseases, such as
CC malignant tumours, nosohaemia, HIV infection, immunological diseases and
CC inflammatory disorder. The present sequence is a probe used to
CC detect polynucleotides encoding the polypeptide of the invention.
XX
SQ Sequence 41 BP; 16 A; 9 G; 11 G; 5 T; 0 other;

Query Match 0.9%; Score 24.6; DB 24; Length 41;
Best Local Similarity 76.9%; Pred. No. 1.7e+03;
Matches 30; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1066 TCACACATCAGAGGACACACCTCAGGGAACCTTATG 1104
DB 1 TGAGACATCAGAGAGTGCACACAGAGAGAAACCTTACG 39

RESULT 40
AAH89252
ID AAH89252 standard; DNA: 51 BP.
AC AAH89252;
XX
XX 01-OCT-2001 (first entry)
DT
XX
DE Human transcription factor DNA polymorphic site SEQ ID NO: 33.
XX
XX Human; single nucleotide polymorphism; SNP; paternity test;
KW forensic test; aberrant protein expression; ds.
XX
XX Homo sapiens.
OS
XX WO200151670-A2.
PN
XX
XX 19-JUL-2001.
PD
XX
XX 05-JAN-2001; 2001WO-US00322.
PF
XX
XX 07-JAN-2000; 2000US-0174962.
PR
XX
XX (CURA-) CURAGEN CORP.
PA
XX
XX Shimkets RA, Leach MD;
PI
XX
XX WPI: 2001-451871/48.
DR
XX
XX P-PSDB: AAM00143.
DR
XX
XX Isolated human polynucleotides containing single nucleotide
PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
XX infection and diabetes -
XX
XX
XX Claim 1; Page 119; 475pp; English.
PS
XX
XX The present invention relates to human nucleic acids containing single
CC nucleotide polymorphisms (SNPs). These can be used in forensic and
CC paternity tests, and to aid in the treatment of diseases associated with
CC aberrant protein expression, including cancer, amyloidosis, diabetes,
CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
CC glomerulonephritis, haemolytic anaemia, thrombocytopenia, arthritis,
CC meningitis, muscular disorders, dementia, neurological diseases, tubercous
CC osteoporosis, pathogenic infections, hypercalcaemia, blood pressure disorders,
CC autoimmunity. The present sequence is a polymorphism-containing
CC oligonucleotide fragment of the invention.
XX
XX
SQ Sequence 51 BP; 13 A; 10 C; 16 G; 12 T; 0 other;

Query Match 0.9%; Score 24.6; DB 22; Length 51;
Best Local Similarity 70.2%; Pred. No. 2e+03;
Matches 33; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1251 CACACTGGGAGAAACCTTATGTTTCAGAGGAATGTGGCGTGTGCTT 1297
DB 4 CACACTGGAGAGAAACCTTATGATGTTTGTGATGTGGAGGCGCTT 50

RESULT 41
AAH89253
ID AAH89253 standard; DNA: 51 BP.
XX
XX
XX AAH89253;
AC

XX	01-OCT-2001 (first entry)	
DT		
XX		
DE	Human transcription factor DNA polymorphic site SEQ ID NO: 34.	
XX		
KM	Human: single nucleotide polymorphism; SNP; paternity test;	
KM	forensic test; aberrant protein expression; ds.	
XX		
OS	Homo sapiens.	
XX		
PN	MO200151670-A2.	
XX		
PD	19-JUL-2001.	
XX		
PF	05-JAN-2001; 2001WO-US00322.	
XX		
PR	07-JAN-2000; 2000US-0174962.	
XX		
PA	(CURA-) CURAGEN CORP.	
XX		
P1	Shimkets RA, Leach MD;	
XX		
DR	WPI: 2001-451871/48.	
XX		
DR	P-PSDB, AAM00144.	
XX		
PT	Isolated human polynucleotides containing single nucleotide	
PT	polymorphisms, useful for the treatment and diagnosis of e.g. cancer,	
PT	infection and diabetes -	
XX		
PS	Claim 1; Page 119; 475pp; English.	
XX		
CC	The present invention relates to human nucleic acids containing single	
CC	nucleotide polymorphisms (SNPs). These can be used in forensic and	
CC	paternity tests, and to aid in the treatment of diseases associated with	
CC	aberrant protein expression, including cancer, amyloidosis, diabetes,	
CC	Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,	
CC	glomerulonephritis, haemolytic anaemia, thrombocytopenia, arthritis,	
CC	meningitis, muscular disorders, dementia, neurological diseases, tubercous	
CC	sclerosis, male infertility, hypercalcaemia, blood pressure disorders,	
CC	osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or	
CC	autoimmunity. The present sequence is a polymorphism-containing	
CC	oligonucleotide fragment of the invention.	
XX		
SQ	Sequence 51 BP; 14 A; 10 C; 15 G; 12 T; 0 other;	
	Query Match 0.9%; Score 24.6; DB 22; Length 51;	
	Best Local Similarity 70.2%; Pred. No. 2e+03;	
	Matches 33; Conservative 0; Mismatches 14; Indels 0; Gaps 0;	
Oy	1251 CACACTGGGAGAACCTTATGTTTCAGAGGAATGCGGCTT 1297	
Db	4 CACACTGGAGAGAAACCTATTAATGTTGTGATGTGGAGAGCCTT 50	
	RESULT 42	
	AAD33628/C	
ID	AAD33628 standard; DNA; 55 BP.	
XX		
AC	AAD33628;	
XX		
DT	01-JUL-2002 (first entry)	
XX		
DE	21f-3 specific antisense oligo used to generate three finger ZFP.	
XX		
KM	DNA binding protein; zinc finger domain 3; zinc finger protein; ZFP;	
KM	viral replication; gene expression; virucide; Z1f3; ss.	
XX		
OS	Unidentified.	
XX		
PN	WO200208286-A2.	
XX		
PD	31-JAN-2002.	
XX		

```

PF 19-JUL-2001; 2001WO-EP08367.
PR XX
XX 21-JUL-2000; 2000US-220060P.
PA XX
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
PI XX
PI Sera T;
XX XX
DR WPI: 2002-172000/22.
XX XX
XX New Zinc Finger Protein (ZFP) comprising three essential domains useful
PT for diagnosing diseases associated with abnormal genomic structure -
PS Example 7; Page 72; 143pp; English.
CC The present invention relates to novel DNA binding proteins comprising
CC zinc finger domains in which two histidine and two cysteine residues
CC coordinate a central zinc ion. The invention particularly relates to
CC the identification of a context-independent recognition code to design
CC zinc finger domains. The invention also relates to zinc finger proteins
CC (ZFP) designed using this recognition code. The ZFPs are useful for
CC altering genomic structure, inhibiting viral replication (where viral
CC replication is inhibited for plant virus, an animal virus or a human
CC virus), modulating gene expression, detecting an altered zinc finger
CC recognition sequence and diagnosing disease associated with abnormal
CC genomic structure. The present DNA sequence is zinc finger domain 3
CC (ZF1-3) specific oligonucleotide which is used to generate three finger
CC ZFP for the I.I site of beet curly top virus (BCTV). This sequence is
CC used in the exemplification of the invention.
SQ Sequence 55 BP; 9 A; 14 C; 15 G; 17 T; 0 other:
Query Match 0.9%; Score 24.6; DB 24; Length 55;
Best Local Similarity 65.5%; Pred. No. 2.1e+03;
Matches 36; Conservative 0; Mismatches 19; Indels 0; Gaps 0
QY 1211 CTTTGGCCGAGTCGAACCGCATTACCACGACGAGCGGCACACTGGGAGAG 1265
||||||| | | | | ||||| | ||||| |||||
DB 55 CTTTAGCTGTACTGATGATGCTTAACAACCCACGACGACGACGAGGGAAGAAG 1
RESULT 43
ABN34011
ID ABN34011 standard; DNA; 60 BP.
XX
XX ABN34011;
AC XX
XX DT 15-JUL-2002 (first entry)
DE Human spliced transcript detection oligonucleotide SEQ ID NO:6759.
XX
XX Human; mouse; rat; splice transcript; detection; RNA transcript;
KM splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
XX WO200210449-A2.
PN XX
PD 07-FEB-2002.
XX
XX 20-JUL-2001; 2001WO-IB01903.
PE
PR 28-JUL-2000; 2000US-221607P.
PR 02-MAY-2001; 2001US-287724P.
XX
PA (COMP-) COMPUGEN INC.
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
XX WPI: 2002-257383/30.
DR
PT New oligonucleotide libraries comprising oligonucleotides which
selectively hybridize to mRNAs transcribed from a transcription unit of

```

PT a genome, useful for detecting tissue-, pathology-, and
 PT developmental-specific genes
 XX
 PS
 XX Example 1: SEQ ID 6759; 47pp; English.

The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNA splice variants. biologically sample, in expression profiling studies, in qualitatively or quantitatively characterising the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised mini libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue- and pathology-specific genes such as those genes only expressed in specific tissue under a specific pathological condition: to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome, and to detect RNA from a particular disorder. ABN27253 to ABN5589 represent oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/publ/abn5589_sequences](http://wipo.int/pub/publ/abn5589_sequences).

Sequence 60 BP; 20 A; 17 C; 9 G; 14 T; 0 other;

```
Query Match      0.98; Score 24.6; DB 24; Length 60;
Best Local Similarity 65.58; Pred. No. 2.2e+03;
Matches 36; Conservative 0; Mismatches 19; Indels 0
```

QY 1375 AAGGCTTTAGCCGAAGTCACACTCATCAGACACTTAAGCAACACACAGAGA 1429
||| ||| ||| | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5 AAGTCTTGAGCCATCATTCATCCCTTAACAGSGACAATTGATGTTTACACCAGACA 59

RESULT 44

ID	standard; DNA; 51 BP.
AA132659	

AC AAL32659;

DT 24-JAN-2002 (first entry)
YY

Human SNP oligonucleotide #5867.

KW Immunosuppressive; immunostimulatory; antinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;
 KW amyloid protein; angiolipolia; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease; ss.

Homo sapiens

WO200147944-A2

05-JUL-2001

28-DEC-2000; 2000WO-US35498.

28-DEC-1999; 99US-0173419.

27-DEC-2000; 2000US-0173419.

(CURA-) CURAGEN CORP.

KX

PI	Shimkets RA, Leach M;
XX	
DR	WPI; 2001-465210/50.
VV	

PT polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections -

PS Claim 1; Page 3073; 4143pp; English.
XY

CC The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiotensin,
CC apoptosis related proteins, cathepsin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC G-protein coupled receptors and thioesterases. The present sequence is
CC one such oligonucleotide. The oligonucleotides and the peptides encoded
CC by them may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate expression of the proteins listed
CC above. Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukemia), diseases of the nervous system and an infection of pathogenic
CC organisms.

50 Sequence 51 BP; 15 A; 6 C; 14 G; 16 T; 0 other;

Query Match	0.98;	Score 24.4;	DB 22;	Length 51;
Best Local Similarity	68.0%;	Pred. No. 2.3e+03;		
Matches 34; Conservative	0;	Mismatches 16;	Totals 0;	Cons 0

QY 1353 TACANTTGCAGGAGCTGTGACGAGCCTTTAGCCGAGAGTCACACCTCAT 1402
|| || ||||||| | ||||||| || |||| | || ||
Db 1 TATAATGTGATGAGTAGTGCGAAGCCTTCAGTCAGACTCAGATCTTAT 50

RESULT 45

ID AAL33200 standard; DNA; 51 BP.

AAC 33200;

DT 24-JAN-2002 (first entry)
XX

Human SNP oligonucleotide #6408.

immunosuppressive; immunostimulatory; antinflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer; amyloid protein; angiotensin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinesin; cytokine; interferon; interleukin; G-protein coupled receptor; thioesterase; inflammation; multifactorial disease; coupled receptor; thioesterase; inflammation; nervous system disease; autoimmune disease; infection; ss.

Homo sapiens.

WO200147944-A2

05-JUL-2001

28-DEC-2000; 2000WO-US35498.

27-DEC-2000: 2000UE-0173419.

27-DEC-2000; 2000US-0173419.

(CURA-) CURAGEN CORP

Shimkets RA, Leach M,

R WPI; 2001-465210/50.

CC messenger RNAs that populate a (sub-)transcriptome, where the
 CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple
 CC transcription units that populate a genome. The library comprises
 CC several oligonucleotides, each capable of hybridising selectively to a
 CC set of messenger RNAs transcribed from a given transcription unit of
 CC the genome, which encodes one or more messenger RNA splice variants.
 CC The oligonucleotide libraries are useful for detecting mRNAs from a
 CC biological sample, in expression profiling studies, in qualitatively or
 CC quantitatively characterising the corresponding transcriptome, and in
 CC detecting RNA transcripts and splice variants of human or animal
 CC transcriptomes. The libraries may also be used as specialised mini
 CC libraries to detect transcripts of a sub-transcriptome under a
 CC particular biological or pathological state, and so allowing the
 CC detection of tissue- and pathology-specific genes such as those genes
 CC only expressed in specific tissue under a specific pathological
 CC condition; to detect developmental specific genes; and to detect RNA
 CC transcripts and splice variants of a transcriptome of a patient suffering
 CC from a particular disorder. ABN27253 to ABN59589 represent
 CC oligonucleotide sequences from rats, humans and mice, which are used in
 CC the exemplification of the present invention.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 60 BP; 20 A; 13 C; 10 G; 17 T; 0 other;

Query Match 0.9%; Score 24.4; DB 24; Length 60;
 Best Local Similarity 63.8%; Pred. No. 2.5e+03;
 Matches 37; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

OY 1337 TTCAGCAGAGAACCTTACATTTGCGAGAGTGTCAGCAGCTTATGCCAGAGTCA 1394
 Db 1 TACTGAGAGCAACCTACATATGTGGAAGAAATGTGTAATTTTACCACATCCTCA 58

RESULT 48

AAH77419
 ID AAH77419 standard; DNA: 41 BP.

XX AAH77419;

DT 05-NOV-2001 (first entry)

DE Human zinc finger protein 32 coding sequence probe #1.

KW Human; zinc finger protein 32; cancer; nervous system disease;
 KW haemopathy; development disorder; HIV infection; immune disorder;
 KW inflammation; gene therapy; probe; ss.

OS Homo sapiens.

PN WO200166731-A1.

PD 13-SEP-2001.

PF 26-FEB-2001; 2001WO-CN00289.

PR 07-MAR-2000; 2000CN-0111915.

PA (BIOV-) BLOWINDOW GENE DEV INC SHANGHAI.

PI Mao Y, Xie Y;

WPI: 2001-557869/62.

PT Human zinc finger protein 32 and encoded polynucleotide, used in
 PT diagnosis and treatment of e.g. nervous system diseases, malignant
 PT tumor, hemopathy, human immunodeficiency virus infection, and
 PT inflammations

XX Example 7; Page 15; 34pp; Chinese.

CC The present invention provides the protein and coding sequences of human

CC zinc finger protein 32. The sequences can be used in the treatment of
 CC cancer, nervous system diseases, haemopathy, development disorders, HIV
 CC infection, immune diseases and inflammation. The present sequence is a
 CC probe for the coding sequence of the invention.

SQ Sequence 41 BP; 18 A; 10 C; 7 G; 6 T; 0 other;

Query Match 0.9%; Score 23.8; DB 22; Length 41;
 Best Local Similarity 80.0%; Pred. No. 3.1e+03;
 Matches 28; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1412 AAGACACACAGAGAGACCTTATGTATGCA 1446
 Db 4 AAAAATCAGACTGAGAGAAACCTATGATGCA 38

RESULT 49

AAI79772/c
 ID AAI79772 standard; DNA: 51 BP.

XX AAI79772;

DT 09-NOV-2001 (first entry)

DE Human nonconservative amino acid changing SNP nucleic acid SEQ:6713.

KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
 KW protein therapy; vaccine; probe; diagnostic assay; detection;
 KW quantitation; restorative therapy; polymorphic; ds.

OS Homo sapiens.

PN WO200140521-A2.

PD 07-JUN-2001.

PF 30-NOV-2000; 2000WO-US32758.

PR 30-NOV-1999; 99US-0168138.

PR 29-NOV-2000; 2000US-0726173.

PA (CURA-) CURAGEN CORP.

PI Shimkets RA, Leach M;

WPI: 2001-356160/37.

PT Polymorphic nucleic acid sequences, useful in genetic testing and
 PT therapy

PS Claim 1; Page 2559; 2653pp; English.

CC AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide
 CC sequences (I), which contain single nucleotide polymorphisms (SNPs).

CC AAM53114 to AAM53329 represent peptides related to human polymorphic
 CC polynucleotide sequences. The sequences can be used in gene and protein
 CC therapy, and in vaccine production. (I) and the polypeptides encoded by
 CC them may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate expression of polymorphic polypeptides.

CC For example, (I) may be used to treat disorders by rectifying mutations
 CC or deletions in a patient's genome that affect the activity of
 CC polypeptides by expressing inactive proteins or to supplement the
 CC patients own production of polypeptide. Additionally, (I) and its
 CC complementary sequences may also be used as DNA probes in diagnostic
 CC assays to detect and quantitate the presence of similar nucleic acids
 CC in samples, and therefore which patients may be in need of restorative
 CC therapy. The polypeptides encoded by (I) may be used as antigens in the
 CC production of antibodies specific for polymorphic polypeptides. The
 CC antibodies may also be used to down regulate expression and activity.

CC The antibodies may also be used as diagnostic agents for detecting the
 CC presence of polymorphic polypeptides in samples.

CC Sequence 51 BP; 15 A; 13 C; 17 G; 6 T; 0 other;

XX

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OM nucleic - nucleic search, using sw model

Run on: June 4, 2003, 05:33:54 ; Search time 7121 seconds

(without alignments)
11328.883 Million cell updates/sec

Title: US-09-898-556a-3

Perfect score: 2772

Sequence: 1 cagcgcgctaagctgctg.....ttctaccatccctaccct 2772

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 897812

Minimum DB seq length: 0

Maximum DB seq length: 60

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrl:*
38: em_sy:*
39: em_hcgo_hum:*
40: em_hcgo_mus:*
41: em_hcgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	49.4	1.8	51.6	AX165270	AX165270 Sequence
C 2	49.4	1.8	51.6	AX165674	AX165674 Sequence
C 3	34.6	1.2	51.6	AX161256	AX161256 Sequence
C 4	33	1.2	51.6	AX161255	AX161255 Sequence
C 5	27.8	1.0	51.6	AX163066	AX163066 Sequence
C 6	27.6	1.0	51.6	AX161706	AX161706 Sequence
C 7	27	1.0	60.6	AX382506	AX382506 Sequence
C 8	26.6	1.0	51.6	AX199456	AX199456 Sequence
C 9	26.6	1.0	56.6	AX382519	AX382519 Sequence
C 10	26.2	0.9	51.6	AX163065	AX163065 Sequence
C 11	26	0.9	51.6	AX161705	AX161705 Sequence
C 12	25.8	0.9	60.6	AX382515	AX382515 Sequence
C 13	25.6	0.9	56.6	AX382510	AX382510 Sequence
C 14	24.6	0.9	51.6	AX199103	AX199103 Sequence
C 15	24.6	0.9	51.6	AX199104	AX199104 Sequence
C 16	24.6	0.9	55.6	AX382520	AX382520 Sequence
C 17	23.8	0.9	51.6	AX163385	AX163385 Sequence
C 18	23.8	0.9	55.6	AX382511	AX382511 Sequence
C 19	23	0.8	51.6	AX159659	AX159659 Sequence
C 20	23	0.8	51.6	AX199545	AX199545 Sequence
C 21	23	0.8	60.6	AX449256	AX449256 Sequence
C 22	22.4	0.8	48.9	HUM2EM	M88369 Homo sapien
C 23	22.4	0.8	60.6	AX382509	AX382509 Sequence
C 24	22.4	0.8	60.6	AX382518	AX382518 Sequence
C 25	22.2	0.8	51.6	AX163386	AX163386 Sequence
C 26	21.8	0.8	51.6	AX115765	AX115765 Sequence
C 27	21.6	0.8	41.6	AR036764	AR036764 Sequence
C 28	21.6	0.8	60.6	AF062523	AF062523 Mus muscu
C 29	21.4	0.8	51.6	AX159660	AX159660 Sequence
C 30	21.4	0.8	60.6	AX449255	AX449255 Sequence
C 31	21.2	0.8	50.6	AX158732	AX158732 Sequence
C 32	21.2	0.8	59.9	HSARD2S16	AF000096 Homo sapi
C 33	21	0.8	31.6	AX249323	AX249323 Sequence
C 34	21	0.8	45.6	AX382526	AX382526 Sequence
C 35	21	0.8	48.6	A84824	A84824 Sequence 19
C 36	21	0.8	50.6	AR107677	AR107677 Sequence
C 37	21	0.8	52.6	AR168446	AR168446 Sequence
C 38	21	0.8	59.6	AR165671	AR165671 Sequence
C 39	20.8	0.8	48.6	A42976	A42976 Sequence 11
C 40	20.8	0.8	48.6	A45522	A45522 Sequence 7
C 41	20.8	0.8	48.6	AR030794	AR030794 Sequence
C 42	20.8	0.8	48.6	AR082131	AR082131 Sequence
C 43	20.8	0.8	51.6	AX165344	AX165344 Sequence
C 44	20.6	0.7	51.6	AX162153	AX162153 Sequence
C 45	20.6	0.7	51.6	AX162154	AX162154 Sequence
C 46	20.6	0.7	52.6	AR165679	AR165679 Sequence
C 47	20.6	0.7	60.9	HUMNME1E	L05010 Homo sapien
C 48	20.4	0.7	51.6	AX158272	AX158272 Sequence
C 49	20.4	0.7	52.10	D50270	D50270 Mouse Pig-f
C 50	20.2	0.7	50.6	AR040811	AR040811 Sequence
C 51	20.2	0.7	52.6	A41832	A41832 Sequence 13
C 52	20.2	0.7	53.6	I24813	I24813 Sequence 2
C 53	20.2	0.7	57.9	S57604	S57604 T-cell - rece
C 54	20.2	0.7	60.6	AX429005	AX429005 Sequence
C 55	20.2	0.7	60.6	I42389	I42389 Sequence 21
C 56	20	0.7	31.6	AX249325	AX249325 Sequence
C 57	20	0.7	48.6	AR000192	AR000192 Sequence
C 58	20	0.7	48.6	AX008144	AX008144 Sequence
C 59	20	0.7	52.6	AX395011	AX395011 Sequence
C 60	20	0.7	52.6	AX184291	AX184291 Sequence
C 61	20	0.7	55.6	AR112996	AR112996 Sequence
C 62	20	0.7	55.6	E49740	E49740 Biological
C 63	20	0.7	55.6	I28996	I28996 Sequence 7
C 64	20	0.7	56.6	AX008143	AX008143 Sequence
C 65	19.8	0.7	47.6	AR110217	AR110217 Sequence

C 66	19.8	0.7	47	6	AR169976	Sequence	C 139	19	0.7	51	6	AX158371	Sequence	AX158371	Sequence
C 67	19.8	0.7	47	6	AR171785	Sequence	C 140	19	0.7	51	6	AX160377	Sequence	AX160377	Sequence
C 68	19.8	0.7	47	6	AX378376	Sequence	C 141	19	0.7	51	6	AX162285	Sequence	AX162285	Sequence
C 69	19.8	0.7	47	6	BD009010	Promoter	C 142	19	0.7	51	6	AX163319	Sequence	AX163319	Sequence
C 70	19.8	0.7	50	6	AX159884	Sequence	C 143	19	0.7	51	6	AX165251	Sequence	AX165251	Sequence
C 71	19.8	0.7	51	6	AX158137	Sequence	C 144	19	0.7	51	6	AX204116	Sequence	AX204116	Sequence
C 72	19.8	0.7	51	6	AX159652	Sequence	C 145	19	0.7	52	8	CNS01Bxv	Sequence	AX14827	Botrytis
C 73	19.8	0.7	51	6	AX160179	Sequence	C 146	19	0.7	54	6	AI3518	Sequence	AI3518	DNA fragment
C 74	19.8	0.7	51	6	AX165672	Sequence	C 147	19	0.7	54	6	A52692	Sequence	A52692	Sequence
C 75	19.8	0.7	57	3	AB032141	Drosophila	C 148	19	0.7	54	9	HUMG3A03	Sequence	M10798	Human alpha
C 76	19.8	0.7	57	6	AR117908	Sequence	C 149	19	0.7	57	6	AA1144	Sequence	AA1144	Sequence
C 77	19.8	0.7	59	6	AX286580	Sequence	C 150	19	0.7	57	6	AR153765	Sequence	AR153765	Sequence
C 78	19.6	0.7	48	6	AX047705	Sequence	C 151	19	0.7	57	9	MTSLA576	Sequence	X89640	H. sapiens m
C 79	19.6	0.7	51	6	AX117637	Sequence	C 152	19	0.7	59	6	AX011337	Sequence	AX011337	Sequence
C 80	19.6	0.7	51	6	AX117789	Sequence	C 153	19	0.7	60	10	AF328233	Sequence	AF328233	Mus muscu
C 81	19.6	0.7	51	6	AX117861	Sequence	C 154	18.8	0.7	40	6	AX079225	Sequence	AX079225	Sequence
C 82	19.6	0.7	51	6	AX157005	Sequence	C 155	18.8	0.7	40	6	AX080067	Sequence	AX080067	Sequence
C 83	19.6	0.7	51	6	AX157006	Sequence	C 156	18.8	0.7	43	6	AR013755	Sequence	AR013755	Sequence
C 84	19.6	0.7	51	6	AX161747	Sequence	C 157	18.8	0.7	43	6	AR013756	Sequence	AR013756	Sequence
C 85	19.6	0.7	51	6	AX190113	Sequence	C 158	18.8	0.7	49	6	AR011505	Sequence	AR011505	Sequence
C 86	19.6	0.7	53	6	I05885	Sequence 2	C 159	18.8	0.7	49	6	AR061800	Sequence	I18143	Sequence 37
C 87	19.6	0.7	53	6	I05930	Sequence 2	C 160	18.8	0.7	50	6	AX093090	Sequence	AX093090	Sequence
C 88	19.6	0.7	53	6	I08801	Sequence 1	C 161	18.8	0.7	50	6	AX161748	Sequence	AX161748	Sequence
C 89	19.6	0.7	53	6	I09164	Sequence 2	C 162	18.8	0.7	50	6	AX158271	Sequence	AX158271	Sequence
C 90	19.6	0.7	53	6	I09610	Sequence 1	C 163	18.8	0.7	51	6	AX158899	Sequence	AX158899	Sequence
C 91	19.6	0.7	56	6	I43365	Sequence 9	C 164	18.8	0.7	51	6	AX160140	Sequence	AX160140	Sequence
C 92	19.6	0.7	56	6	I61420	Sequence 9	C 165	18.8	0.7	51	6	AX160496	Sequence	AX160496	Sequence
C 93	19.6	0.7	56	6	I96034	Sequence 9	C 166	18.8	0.7	51	6	AX199398	Sequence	AX199398	Sequence
C 94	19.6	0.7	59	3	S59976	TAL1d2-prot	C 167	18.8	0.7	51	6	AX204439	Sequence	AX204439	Sequence
C 95	19.6	0.7	59	3	AR411985	Formica e	C 168	18.8	0.7	51	6	AX304454	Sequence	AX304454	Sequence
C 96	19.6	0.7	59	6	I09611	Sequence 2	C 169	18.8	0.7	54	6	A22726	Sequence	A22726	synthetic f
C 97	19.6	0.7	59	6	S43435S10	Transmembr	C 170	18.8	0.7	54	6	A47685	Sequence	A47685	Sequence 3
C 98	19.6	0.7	60	6	AR163465	Sequence	C 171	18.8	0.7	54	6	AX135220	Sequence	AX135220	Sequence
C 99	19.6	0.7	60	6	AR163466	Sequence	C 172	18.8	0.7	54	6	BD006609	Process f	BD006609	Process f
C 100	19.4	0.7	33	6	BD010994	HIV probe	C 173	18.8	0.7	54	6	I07497	Sequence 3	I07497	Sequence 3
C 101	19.4	0.7	45	6	AX382524	Sequence	C 174	18.8	0.7	54	6	I21368	Sequence 6	I21368	Sequence 6
C 102	19.4	0.7	48	10	MUSIGHZ	Mouse Ig ge	C 175	18.8	0.7	54	6	HSTCEL16	Sequence	X81551	H. sapiens r
C 103	19.4	0.7	50	6	AX159889	Sequence	C 176	18.8	0.7	56	6	AX061289	Sequence	AX061289	Sequence
C 104	19.4	0.7	51	6	PF246197S02	Rattus no	C 177	18.8	0.7	59	3	AF411985	Sequence	AF411985	Formica e
C 105	19.4	0.7	51	6	AX156932	Sequence	C 178	18.8	0.7	59	6	AX150275	Sequence	AX150275	Sequence
C 106	19.4	0.7	51	6	AX162214	Sequence	C 179	18.8	0.7	60	9	HUMSAU3A04	Sequence	D49588	Human alpha
C 107	19.4	0.7	55	9	AX204400	Sequence	C 180	18.8	0.7	60	9	HUMSAU3A61	Sequence	D49645	Human alpha
C 108	19.4	0.7	55	9	S76405	PML-RARA fl.	C 181	18.8	0.7	25	6	AR207599	Sequence	E50868	Gene inhibi
C 109	19.4	0.7	57	9	AF011607	Homo sapi.	C 182	18.6	0.7	36	6	E50868	Sequence	S59762	IgVH-pre-B-
C 110	19.4	0.7	57	9	AF011639	Homo sapi.	C 183	18.6	0.7	36	6	AR041498	Sequence	AR159578	Sequence
C 111	19.4	0.7	59	6	A84789	Sequence 34	C 184	18.6	0.7	39	6	A70765	Sequence	A70765	Sequence
C 112	19.2	0.7	41	6	A58755	Sequence 1	C 185	18.6	0.7	39	6	BD003479	Sequence	BD003479	A gene re
C 113	19.2	0.7	44	6	AR118799	Sequence	C 186	18.6	0.7	42	6	AR031386	Sequence	BD009754	Compositi
C 114	19.2	0.7	45	6	AR032488	Sequence	C 187	18.6	0.7	43	6	AX010673	Sequence	AX010673	Sequence
C 115	19.2	0.7	45	6	AR209152	Sequence	C 188	18.6	0.7	45	6	A40447	Sequence 74	A40447	Sequence 74
C 116	19.2	0.7	45	6	I29228	Sequence 10	C 189	18.6	0.7	48	10	AB001352	Sequence 16	AB001352	Mus muscu
C 117	19.2	0.7	45	6	I90902	Sequence 10	C 190	18.6	0.7	50	6	AX160044	Sequence	AX160044	Sequence
C 118	19.2	0.7	48	6	AR176079	Sequence	C 191	18.6	0.7	50	10	AF357500	Mus muscu	AF357500	Mus muscu
C 119	19.2	0.7	50	9	AF156531	Homo sapi.	C 192	18.6	0.7	51	6	AX115065	Sequence	AX115065	Sequence
C 120	19.2	0.7	51	6	AX158417	Sequence	C 193	18.6	0.7	51	6	AX157068	Sequence	AX157068	Sequence
C 121	19.2	0.7	51	6	AX158418	Sequence	C 194	18.6	0.7	51	6	AX157497	Sequence	AX157497	Sequence
C 122	19.2	0.7	51	6	AX159317	Sequence	C 195	18.6	0.7	51	6	AX157547	Sequence	AX157547	Sequence
C 123	19.2	0.7	51	6	AX160401	Sequence	C 196	18.6	0.7	51	6	AX157708	Sequence	AX157708	Sequence
C 124	19.2	0.7	51	6	AX162197	Sequence	C 197	18.6	0.7	51	6	AX157900	Sequence	AX157900	Sequence
C 125	19.2	0.7	57	9	HSN224240	Sequence	C 198	18.6	0.7	51	6	AX157905	Sequence	AX157905	Sequence
C 126	19.2	0.7	58	6	AR061277	Homo sapi.	C 199	18.6	0.7	47	6	AR126937	Sequence	AR126937	Sequence
C 127	19.2	0.7	59	6	AR125099	Sequence	C 200	18.6	0.7	48	10	I15842	Sequence 16	I15842	Sequence 16
C 128	19.2	0.7	30	6	AX057116	Sequence	C 201	18.6	0.7	48	10	AB001352	Mus muscu	AB001352	Mus muscu
C 129	19	0.7	31	6	AX249326	Sequence	C 202	18.6	0.7	50	6	AF357500	Mus muscu	AF357500	Mus muscu
C 130	19	0.7	35	6	E32613	Novel nucle	C 203	18.6	0.7	51	6	AX115065	Sequence	AX115065	Sequence
C 131	19	0.7	38	6	AR045392	Sequence	C 204	18.6	0.7	51	6	AX157068	Sequence	AX157068	Sequence
C 132	19	0.7	38	6	I52444	Sequence 18	C 205	18.6	0.7	51	6	AX157497	Sequence	AX157497	Sequence
C 133	19	0.7	45	6	AX283698	Sequence	C 206	18.6	0.7	51	6	AX157547	Sequence	AX157547	Sequence
C 134	19	0.7	46	6	AX259763	Sequence	C 207	18.6	0.7	51	6	AX157708	Sequence	AX157708	Sequence
C 135	19	0.7	48	6	AX382513	Sequence	C 208	18.6	0.7	51	6	AX157900	Sequence	AX157900	Sequence
C 136	19	0.7	48	6	AX426837	Sequence	C 209	18.6	0.7	51	6	AX157905	Sequence	AX157905	Sequence
C 137	19	0.7	49	10	S79631S3	HSF2-heat s	C 210	18.6	0.7	51	6	AX158419	Sequence	AX158419	Sequence
C 138	19	0.7	51	6	AX117289	Sequence	C 211	18.6	0.7	51	6	AX160043	Sequence	AX160043	Sequence

212	18.6	0.7	51	6	AX165218	Sequence	285	18.2	0.7	51	6	AX160397	Sequence
213	18.6	0.7	51	6	AX165657	Sequence	286	18.2	0.7	51	6	AX160457	Sequence
214	18.6	0.7	51	6	AX165664	Sequence	287	18.2	0.7	51	6	AX162950	Sequence
215	18.6	0.7	51	6	AX189822	Sequence	288	18.2	0.7	51	6	AX163333	Sequence
216	18.6	0.7	54	10	AA0445	Sequence 72	289	18.2	0.7	51	6	AX165384	Sequence
217	18.6	0.7	54	10	AF328257	Mus muscu	290	18.2	0.7	51	6	AX165613	Sequence
218	18.6	0.7	58	9	HSTNFR2508		291	18.2	0.7	51	6	AX165676	Sequence
219	18.6	0.7	59	9	SS9925	U52163 Human tumor	292	18.2	0.7	51	6	AX165676	Sequence
220	18.4	0.7	29	6	AX080003	SS9925 TAL1d1=prot	293	18.2	0.7	51	6	AX199233	Sequence
221	18.4	0.7	29	6	E09318	E09318 Primer 9/1	294	18.2	0.7	51	6	AX204366	Sequence
222	18.4	0.7	31	6	AR151117	Sequence	295	18.2	0.7	51	9	HUMDC04M3	
223	18.4	0.7	38	6	AX24002	Sequence	296	18.2	0.7	51	10	HUMCTVARA	
224	18.4	0.7	39	6	AX229635	Sequence	297	18.2	0.7	51	13	AF375545	
225	18.4	0.7	40	9	S71320	AX229635 Sequence	298	18.2	0.7	54	6	AX254831	Sequence
226	18.4	0.7	42	6	AR144905	S71320 cystic fibr	299	18.2	0.7	54	6	AX254832	
227	18.4	0.7	42	6	I43221	AX14905 Sequence	300	18.2	0.7	54	6	AX254831	Sequence
228	18.4	0.7	45	6	AR164192	I43221 Sequence 39	301	18.2	0.7	54	6	AR043994	
229	18.4	0.7	48	6	AX222266	Sequence	302	18.2	0.7	56	6	AX089726	Sequence
230	18.4	0.7	48	6	HS4235211	AX222266 Sequence	303	18.2	0.7	56	6	AX089727	Sequence
231	18.4	0.7	49	9	I31449	AJ235211 Homo sapi	304	18.2	0.7	56	6	AX090182	Sequence
232	18.4	0.7	50	6	A78547	I31449 Sequence 36	305	18.2	0.7	56	6	AX184575	Sequence
233	18.4	0.7	50	6	AR016288	A78547 Sequence 4	306	18.2	0.7	57	5	SMOACGB	
234	18.4	0.7	50	6	AR016288	AR016288 Sequence	307	18.2	0.7	57	5	AX148297	Sequence
235	18.4	0.7	50	6	I60387	AX162646 Sequence	308	18.2	0.7	58	6	MTHSLA598	
236	18.4	0.7	51	6	AR086105	Sequence 4	309	18.2	0.7	60	6	A76630	
237	18.4	0.7	51	6	AX116225	AR086105 Sequence	310	18.2	0.7	60	6	AR097345	Sequence
238	18.4	0.7	51	6	AX157831	Sequence	311	18.2	0.7	60	9	HUMSAU3A12	
239	18.4	0.7	51	6	AX161100	AX157831 Sequence	312	18.2	0.7	60	9	HUMSAU3A35	
240	18.4	0.7	51	6	AX161690	AX161100 Sequence	313	18.2	0.7	60	12	SYNICMAB	
241	18.4	0.7	51	6	AX164840	AX161690 Sequence	314	18	0.6	21	6	AX096028	Sequence
242	18.4	0.7	53	6	A69641	AX164840 Sequence	315	18	0.6	21	6	AX096030	Sequence
243	18.4	0.7	54	6	A38983	A69641 Sequence 2	316	18	0.6	26	6	AX281568	Sequence
244	18.4	0.7	54	6	A38984	A38983 Sequence 70	317	18	0.6	26	6	AX281568	Sequence
245	18.4	0.7	54	6	AR054379	A38984 Sequence 71	318	18	0.6	30	6	AX464694	Sequence
246	18.4	0.7	54	6	AR054380	AR054379 Sequence	319	18	0.6	35	6	AX283309	Sequence
247	18.4	0.7	54	10	MUSICHXR	AR054380 Sequence	320	18	0.6	35	6	AR063739	Sequence
248	18.4	0.7	60	1	CGPROM75	M13400 Mouse Ig ac	321	18	0.6	36	6	I30102	
249	18.4	0.7	60	6	AX369291	X90365 C.glutamicu	322	18	0.6	36	6	AR030428	Sequence
250	18.2	0.7	31	6	BD002595	AX369291 Sequence	323	18	0.6	36	6	AR030446	Sequence
251	18.2	0.7	34	6	AR091831	BD002595 Gene comp	324	18	0.6	36	6	AR030452	Sequence
252	18.2	0.7	34	6	AR157739	AR091831 Sequence	325	18	0.6	36	6	I15726	
253	18.2	0.7	35	6	A90731	AR157739 Sequence	326	18	0.6	37	6	I21496	Sequence 1
254	18.2	0.7	41	6	AX456312	A90731 Sequence 15	327	18	0.6	39	9	S77756	Sequence 43
255	18.2	0.7	41	6	AX327057	AX456312 Sequence	328	18	0.6	43	6	AR004648	Sequence
256	18.2	0.7	42	6	AR127961	AX327057 Sequence	329	18	0.6	43	6	AR034560	Sequence
257	18.2	0.7	45	6	AX040753	AR127961 Sequence	330	18	0.6	45	6	I89250	Sequence
258	18.2	0.7	45	6	AX195145	AX040753 Sequence	331	18	0.6	45	6	AR032684	Sequence 11
259	18.2	0.7	46	6	AX403352	AX195145 Sequence	332	18	0.6	45	6	AR209348	Sequence
260	18.2	0.7	47	6	A38852	AX403352 Sequence	333	18	0.6	45	6	AX306498	Sequence
261	18.2	0.7	47	6	AR174681	A38852 Sequence 6	334	18	0.6	45	6	I29424	Sequence
262	18.2	0.7	48	6	AR165629	AR174681 Sequence	335	18	0.6	45	6	I55019	Sequence 29
263	18.2	0.7	48	6	AX221438	AR165629 Sequence	336	18	0.6	45	6	I91098	Sequence 43
264	18.2	0.7	48	6	AX282194	AX221438 Sequence	337	18	0.6	45	6	AR013876	Sequence 29
265	18.2	0.7	48	6	AX282303	AX282194 Sequence	338	18	0.6	49	6	AR033830	Sequence
266	18.2	0.7	48	6	AX322954	AX282303 Sequence	339	18	0.6	49	6	AR042490	Sequence
267	18.2	0.7	48	6	AX363268	AX322954 Sequence	340	18	0.6	49	6	AR055555	Sequence
268	18.2	0.7	48	6	AX426599	AX363268 Sequence	341	18	0.6	49	6	AR058370	Sequence
269	18.2	0.7	48	6	E02126	AX426599 Sequence	342	18	0.6	49	6	AR082739	Sequence
270	18.2	0.7	50	6	AR148167	E02126 Polylinker	343	18	0.6	49	6	AR084881	Sequence
271	18.2	0.7	50	6	AX160040	AR148167 Sequence	344	18	0.6	49	6	AR087689	Sequence
272	18.2	0.7	50	6	AX160042	AX160040 Sequence	345	18	0.6	49	6	AR088196	Sequence
273	18.2	0.7	50	6	AX199546	AX160042 Sequence	346	18	0.6	49	6	AR094049	Sequence
274	18.2	0.7	50	6	I42228	AX199546 Sequence	347	18	0.6	49	6	AX077279	Sequence
275	18.2	0.7	50	14	RHCNAN	I42228 Sequence 41	348	18	0.6	50	6	AX159802	Sequence
276	18.2	0.7	51	6	AX010669	V01206 Vesicular S	349	18	0.6	51	6	A57490	Sequence
277	18.2	0.7	51	6	AX157231	AX010669 Sequence	350	18	0.6	51	6	AR112992	Sequence 14
278	18.2	0.7	51	6	AX158138	AX157231 Sequence	351	18	0.6	51	6	AX115589	Sequence
279	18.2	0.7	51	6	AX158434	AX158138 Sequence	352	18	0.6	51	6	AX118013	Sequence
280	18.2	0.7	51	6	AX159651	AX158434 Sequence	353	18	0.6	51	6	AX118101	Sequence
281	18.2	0.7	51	6	AX160010	AX159651 Sequence	354	18	0.6	51	6	AX159785	Sequence
282	18.2	0.7	51	6	AX160039	AX160010 Sequence	355	18	0.6	51	6	AX159937	Sequence
283	18.2	0.7	51	6	AX160041	AX160039 Sequence	356	18	0.6	51	6	AX159938	Sequence
284	18.2	0.7	51	6	AX160109	AX160041 Sequence	357	18	0.6	51	6	AX190112	Sequence

C 356	18	0.6	51	6	AX199609	AX199609 Sequence	C 431	17.8	0.6	51	6	AR160586	AR160586 Sequence
C 355	18	0.6	51	6	AX199611	AX199611 Sequence	C 432	17.8	0.6	51	6	AX116289	AX116289 Sequence
C 360	18	0.6	51	6	AX199613	AX199613 Sequence	C 433	17.8	0.6	51	6	AX116529	AX116529 Sequence
C 361	18	0.6	51	6	AX204092	AX204092 Sequence	C 434	17.8	0.6	51	6	AX156931	AX156931 Sequence
C 362	18	0.6	51	6	AX204196	AX204196 Sequence	C 435	17.8	0.6	51	6	AX157592	AX157592 Sequence
C 363	18	0.6	51	6	E61342	E61342 Probe for d	C 436	17.8	0.6	51	6	AX157742	AX157742 Sequence
C 364	18	0.6	51	6	MM090451	U90451 Mus muscul.	C 437	17.8	0.6	51	6	AX158529	AX158529 Sequence
C 365	18	0.6	52	6	A50699	A50699 Sequence 38	C 438	17.8	0.6	51	6	AX158530	AX158530 Sequence
C 366	18	0.6	52	6	AR083330	AR083330 Sequence	C 439	17.8	0.6	51	6	AX162213	AX162213 Sequence
C 367	18	0.6	54	6	AR080277	AR080277 Sequence	C 440	17.8	0.6	51	6	AX163002	AX163002 Sequence
C 368	18	0.6	54	6	AR205535	AR205535 Sequence	C 441	17.8	0.6	51	6	AX163033	AX163033 Sequence
C 369	18	0.6	54	6	AX076553	AX076553 Sequence	C 442	17.8	0.6	51	6	AX163371	AX163371 Sequence
C 370	18	0.6	54	6	AX303573	AX303573 Sequence	C 443	17.8	0.6	51	6	AX163372	AX163372 Sequence
C 371	18	0.6	54	9	S81114	S81114 Homo sapien	C 444	17.8	0.6	51	6	AX164986	AX164986 Sequence
C 372	18	0.6	55	6	AR088559	AR088559 Sequence	C 445	17.8	0.6	51	6	AX165059	AX165059 Sequence
C 373	18	0.6	55	6	AX485745	AX485745 Sequence	C 446	17.8	0.6	51	6	AX165249	AX165249 Sequence
C 374	18	0.6	56	9	CEBSAT4	M19458 C.apella sa	C 447	17.8	0.6	51	6	AX165542	AX165542 Sequence
C 375	18	0.6	56	17	HSMC09F1	X86429 H.sapiens D	C 448	17.8	0.6	51	6	AX165770	AX165770 Sequence
C 376	18	0.6	58	6	AX148295	AX148295 Sequence	C 449	17.8	0.6	51	6	AX203999	AX203999 Sequence
C 377	18	0.6	59	6	BD001710	BD001710 Compositi	C 450	17.8	0.6	51	6	AX204300	AX204300 Sequence
C 378	18	0.6	59	6	BD001723	BD001723 Method fo	C 451	17.8	0.6	51	6	AX322220	AX322220 Sequence
C 379	18	0.6	60	6	AR117072	AR117072 Sequence	C 452	17.8	0.6	51	14	AF233180	AF233180 Human pol
C 380	18	0.6	60	6	AX027956	AX027956 Sequence	C 453	17.8	0.6	51	14	AF233185	AF233185 Human pol
C 381	18	0.6	60	6	AX060089	AX060089 Sequence	C 454	17.8	0.6	52	6	AR203026	AR203026 Sequence
C 382	18	0.6	60	6	I05516	I05516 Sequence	C 455	17.8	0.6	52	6	AX183597	AX183597 Sequence
C 383	18	0.6	60	6	I09144	I09144 Sequence 4	C 456	17.8	0.6	54	6	AR041224	AR041224 Sequence
C 384	18	0.6	60	6	I20529	I20529 Sequence 72	C 457	17.8	0.6	54	6	AR059169	AR059169 Sequence
C 385	18	0.6	60	8	CNS0190C3	AL111459 Botrytis	C 458	17.8	0.6	54	6	AR135485	AR135485 Sequence
C 386	18	0.6	60	12	AX028053	AX028053 Sequence	C 459	17.8	0.6	54	6	AR203062	AR203062 Sequence
C 387	18	0.6	60	14	SHTRANSLSA	M27001 Suid herpes	C 460	17.8	0.6	54	6	I18975	I18975 Sequence 57
C 388	17.8	0.6	28	6	AR092331	AR092331 Sequence	C 461	17.8	0.6	54	6	I24160	I24160 Sequence 57
C 389	17.8	0.6	30	6	AR000099	AR000099 Sequence	C 462	17.8	0.6	54	6	I65516	I65516 Sequence 12
C 390	17.8	0.6	30	6	AR064922	AR064922 Sequence	C 463	17.8	0.6	54	10	MM090498	MM090498 Mus muscul
C 391	17.8	0.6	31	6	AX249324	AX249324 Sequence	C 464	17.8	0.6	56	9	AF067416	AF067416 Homo sapi
C 392	17.8	0.6	38	6	AR045384	AR045384 Sequence	C 465	17.8	0.6	57	6	AR127689	AR127689 Sequence
C 393	17.8	0.6	38	6	AR045386	AR045386 Sequence	C 466	17.8	0.6	57	6	I75358	I75358 Sequence 10
C 394	17.8	0.6	38	6	AR148761	AR148761 Sequence	C 467	17.8	0.6	58	6	I28251	I28251 Sequence 9
C 395	17.8	0.6	38	6	AX273588	AX273588 Sequence	C 468	17.8	0.6	59	6	AR052201	AR052201 Sequence
C 396	17.8	0.6	38	6	I52436	I52436 Sequence 17	C 469	17.8	0.6	59	6	AX474322	AX474322 Sequence
C 397	17.8	0.6	38	6	I52448	I52448 Sequence 16	C 470	17.8	0.6	60	6	AI18945	AI18945 Oligonucleo
C 398	17.8	0.6	40	6	AX456405	AX456405 Sequence	C 471	17.8	0.6	60	6	AI19031	AI19031 Nucleotide
C 399	17.8	0.6	43	6	AR011922	AR011922 Sequence	C 472	17.8	0.6	60	6	AI19032	AI19032 Nucleotide
C 400	17.8	0.6	43	6	AR017793	AR017793 Sequence	C 473	17.8	0.6	60	6	A29222	A29222 Oligonucleo
C 401	17.8	0.6	43	6	AR077198	AR077198 Sequence	C 474	17.8	0.6	60	6	AR097344	AR097344 Sequence
C 402	17.8	0.6	43	6	E38119	E38119 DNA elongat	C 475	17.8	0.6	60	6	AX365977	AX365977 Sequence
C 403	17.8	0.6	45	6	AR125138	AR125138 Sequence	C 476	17.8	0.6	60	6	AX382507	AX382507 Sequence
C 404	17.8	0.6	45	6	AR147495	AR147495 Sequence	C 477	17.8	0.6	60	6	E22154	E22154 Yeast capab
C 405	17.8	0.6	45	6	AX236658	AX236658 Sequence	C 478	17.8	0.6	60	9	HSEARING16	AF053446 Homo sapi
C 406	17.8	0.6	45	6	E14204	E14204 PCR primer	C 479	17.8	0.6	60	9	H0MSA03A58	D49642 Human alipho
C 407	17.8	0.6	46	12	STNGALAD	M10294 Bacterophing	C 480	17.8	0.6	27	6	AR184790	AR184790 Sequence
C 408	17.8	0.6	47	6	AR036878	AR036878 Sequence	C 481	17.6	0.6	28	6	I11732	I11732 Sequence 3
C 409	17.8	0.6	47	6	AR036885	AR036885 Sequence	C 482	17.6	0.6	32	6	AX320735	AX320735 Sequence
C 410	17.8	0.6	47	6	AR088352	AR088352 Sequence	C 483	17.6	0.6	32	6	S9555782	S95559 B-raf-proto
C 411	17.8	0.6	47	6	AX194680	AX194680 Sequence	C 484	17.6	0.6	33	6	AX225260	AX225260 Sequence
C 412	17.8	0.6	47	6	AX194718	AX194718 Sequence	C 485	17.6	0.6	33	6	AX317243	AX317243 Sequence
C 413	17.8	0.6	47	6	I30213	I30213 Sequence 6	C 486	17.6	0.6	35	6	AR134889	AR134889 Sequence
C 414	17.8	0.6	47	6	I41063	I41063 Sequence 6	C 487	17.6	0.6	35	6	AR182309	AR182309 Sequence
C 415	17.8	0.6	48	6	A78686	A78686 Sequence 3	C 488	17.6	0.6	35	6	I81283	I81283 Sequence 34
C 416	17.8	0.6	48	6	A78687	A78687 Sequence 4	C 489	17.6	0.6	36	6	A17744	A17744 Nucleotide
C 417	17.8	0.6	48	6	AX081679	AX081679 Sequence	C 490	17.6	0.6	36	6	AR058429	AR058429 Sequence
C 418	17.8	0.6	48	6	AX222045	AX222045 Sequence	C 491	17.6	0.6	36	6	AR058430	AR058430 Sequence
C 419	17.8	0.6	48	6	E40904	E40904 Humanized a	C 492	17.6	0.6	36	6	AR133439	AR133439 Sequence
C 420	17.8	0.6	48	10	MUSGIMZB	M23398 Mouse Ig 3e	C 493	17.6	0.6	36	6	E14547	E14547 DNA probe f
C 421	17.8	0.6	49	6	AR153115	AR153115 Sequence	C 494	17.6	0.6	36	6	I11602	I11602 Sequence 27
C 422	17.8	0.6	49	6	AR153116	AR153116 Sequence	C 495	17.6	0.6	36	6	I35123	I35123 Sequence 91
C 423	17.8	0.6	49	6	AR210916	AR210916 Sequence	C 496	17.6	0.6	37	6	I04708	I04708 Sequence 32
C 424	17.8	0.6	49	6	AR210917	AR210917 Sequence	C 497	17.6	0.6	38	6	AX076796	AX076796 Sequence
C 425	17.8	0.6	49	6	AX259764	AX259764 Sequence	C 498	17.6	0.6	39	6	AR208355	AR208355 Sequence
C 426	17.8	0.6	49	6	AX356710	AX356710 Sequence	C 499	17.6	0.6	41	6	AR036778	AR036778 Sequence
C 427	17.8	0.6	49	6	AX356711	AX356711 Sequence	C 500	17.6	0.6	41	6	BD012559	BD012559 Method of
C 428	17.8	0.6	49	6	AX361211	AX361211 Sequence							
C 429	17.8	0.6	50	6	AX161238	AX161238 Sequence							
C 430	17.8	0.6	50	6	AX165814	AX165814 Sequence							

ALIGNMENTS

RESULT 1
AXI65270/c
LOCUS AXI65270 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 465 from Patent WO0138586.
ACCESSION AXI65270
VERSION AXI65270.1 GI:14546099
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 51)
TITLE Shinkets, R.A. and Leach, M.
Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0138586-A 465 31-MAY-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
1..51
/organism="Homo sapiens"
/db_xref="taxon:9606"
variation
26
/note="single nucleotide polymorphism
Accession number C943297259"
BASE COUNT 9 a 10 c 14 g 18 t
ORIGIN
Query Match 1.8%; Score 49.4; DB 6; Length 51;
Best Local Similarity 98.0%; Pred. No. 0.002;
Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DB 1378 GCTTAGCCAGAGTCACACCTCATCAGACTTAAGCAGACACAGAG 1428
51 GCTTAGCCAGAGTCACACCTCATCAGACTTAAGCAGACACAGAG 1

RESULT 2
AXI65674/c
LOCUS AXI65674 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 869 from Patent WO0138586.
ACCESSION AXI65674
VERSION AXI65674.1 GI:14546503
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 51)
TITLE Shinkets, R.A. and Leach, M.
Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0138586-A 869 31-MAY-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
1..51
/organism="Homo sapiens"
/db_xref="taxon:9606"
variation
26
/note="single nucleotide polymorphism
Accession number C943297259"
BASE COUNT 10 a 14 c 12 g 15 t
ORIGIN
Query Match 1.8%; Score 49.4; DB 6; Length 51;
Best Local Similarity 98.0%; Pred. No. 0.002;
Matches 50; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DB 1362 AGGAGGTGAGCAGAGCTTATGAGCAGAGTACACACTCATCAGACTTA 1412
51 AGGAGGTGAGCAGAGCTTATGAGCAGAGTACACACTCATCAGACTTA 1

RESULT 3
AXI61256
LOCUS AXI61256 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 4584 from Patent WO0140521.
ACCESSION AXI61256
VERSION AXI61256.1 GI:14542587
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 51)
TITLE Shinkets, R.A. and Leach, M.
Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 4584 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
1..51
/organism="Homo sapiens"
/db_xref="taxon:9606"
misc_feature
26
/note="2 of 2 allelic variants (4583 is other entry)
Accession number C943960167"
BASE COUNT 17 a 14 c 13 g 7 t
ORIGIN
Query Match 1.2%; Score 34.6; DB 6; Length 51;
Best Local Similarity 81.6%; Pred. No. .78;
Matches 40; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
DB 2375 AGTCAAAATGCCAGGAGATAGGGGTGACTGTGTAACCCAACT 2423
1 AGTCAAAATGCCAGGAGATAGGGGTGACTGTGTAACCCAACT 49

RESULT 4
AXI61255
LOCUS AXI61255 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 4583 from Patent WO0140521.
ACCESSION AXI61255
VERSION AXI61255.1 GI:14542586
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 51)
TITLE Shinkets, R.A. and Leach, M.
Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 4583 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
1..51
/organism="Homo sapiens"
/db_xref="taxon:9606"
misc_feature
26
/note="1 of 2 allelic variants (4584 is other entry)
Accession number C943960167"
BASE COUNT 17 a 15 c 13 g 6 t
ORIGIN
Query Match 1.2%; Score 33; DB 6; Length 51;
Best Local Similarity 79.6%; Pred. No. 2.5e+02;
Matches 39; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
DB 2375 AGTCAAAATGCCAGGAGATAGGGGTGACTGTGTAACCCAACT 2423
1 AGTCAAAATGCCAGGAGATAGGGGTGACTGTGTAACCCAACT 49

[illegible]

LOCUS	AX382506	60 bp	DNA	linear	PAT 18-MAR-2002
DEFINITION	Sequence 36 from Patent WO0208286.				
ACCESSION	AX382506				
VERSION	AX382506.1	GI:19577257			
KEYWORDS					
SOURCE					
ORGANISM	synthetic construct.				
REFERENCE	1	artificial sequences.			
AUTHORS	Sera, T.				
TITLE	zinc finger domain recognition code and uses thereof				
JOURNAL	Patent: WO 0208286-A 36 31-JAN-2002;				
	Syngenta Participations AG (CH)				
FEATURES	Location/Qualifiers				
source	1..60				
	/organism="synthetic construct"				
	/db_xref="taxon:32630"				
	/note="Partial zinc finger domain oligomer."				
BASE COUNT	15 a 6 c 17 g 13 t 9 others				
ORIGIN					
Query Match	1.0%: Score 27; DB 6; Length 60;				
Best Local Similarity	60.0%: Pred. No. 1,8e+04;				
Matches	36; Conservative 0; Mismatches 24; Indels 0; Gaps 0;				
Db	1593 GGGGAGAGCCATTGTATGACGAGTGTGGCGGAGCGCTTACCGGAATCAACCTG 16522				
	1 GGGGAGAGCCGCTTAATGATGCGGAAATGTGTAAGTTTACGNNNAGNNNNNTTG 60				
RESULT 8					
AX199456/c	51 bp	DNA	linear	PAT 29-AUG-2001	
LOCUS	AX199456				
DEFINITION	Sequence 386 from Patent WO0151670.				
ACCESSION	AX199456				
VERSION	AX199456.1	GI:15389859			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
REFERENCE	1 (bases 1 to 51)				
AUTHORS	Shinketsu, R.A. and Leach, M.D.				
TITLE	Nucleic acids containing single nucleotide polymorphisms and				
	methods of use thereof				
JOURNAL	Patent: WO 0151670-A 386 19-JUL-2001;				
	Curagen Corporation (US)				
FEATURES	Location/Qualifiers				
source	1..51				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
misc_feature	26				
	/note="2 of 2 allelic variants (385 is other entry)"				
	Accession number C943300708"				
BASE COUNT	6 a 13 c 23 g 9 t				
ORIGIN					
Query Match	1.0%: Score 26.6; DB 6; Length 51;				
Best Local Similarity	71.4%: Pred. No. 2.4e+04;				
Matches	33; Conservative 0; Mismatches 14; Indels 0; Gaps 0;				
Db	1960 GCTTTACCGCGGAGTCACACCTCATTTAGACACGAGACACATTCAGG 2008				
	49 GCTTACACCGCGCCCTCGCACCTGCTGGCGCACACGAGGACTCACACAG 1				
RESULT 9					
AX382519	56 bp	DNA	linear	PAT 18-MAR-2002	
LOCUS	AX382519				
DEFINITION	Sequence 49 from Patent WO0208286.				
ACCESSION	AX382519				
VERSION	AX382519.1	GI:19577270			

KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.

REFERENCE
1
AUTHORS Sera, T.
TITLE Zinc finger domain recognition code and uses thereof
JOURNAL Patent: WO 0208286-A 49 31-JAN-2002;
Syngenta Participations AG (CH)
FEATURES
source
1.56
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Partial zinc finger domain oligomer."
BASE COUNT 15 a 10 c 19 g 12 t
ORIGIN

Query Match 1.0%; Score 26.6; DB 6; Length 56;
Best Local Similarity 71.4%; Pred. No. 2.4e+04;
Matches 35; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 921 GGGGAGACACCTTACATGTACACTGAGTGGGAGACAGCTTTGGCACTA 969
1 GGGGAGAGCCTTACAGTGCCTGATGCGGAGAGAGCTTTAGTCGTA 49

RESULT 10
AX163065
LOCUS AX163065 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 6393 from Patent WO0140521.
ACCESSION AX163065
VERSION AX163065.1 GI:14544396
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 51)
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Zinc finger domain recognition code and uses thereof
JOURNAL Patent: WO 0140521-A 6393 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source
1.51
/organism="Homo sapiens"
/db_xref="taxon:9606"
misc-feature
26
/note="1 of 2 allelic variants (6394 is other entry)
Accession number C943926631"
BASE COUNT 16 a 7 c 18 g 10 t
ORIGIN

Query Match 0.9%; Score 26.2; DB 6; Length 51;
Best Local Similarity 72.3%; Pred. No. 3.2e+04;
Matches 34; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1243 AGAGGCGCACACTGGGAGAGCCCTTATGTTGCGAGGAATCTGGC 1289
1 AGAGAGTCCACACTGGAGAGAAACCTATAGATGTTGGATCTGGC 47

RESULT 11
AX161705/c
LOCUS AX161705 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 5033 from Patent WO0140521.
ACCESSION AX161705
VERSION AX161705.1 GI:14543036
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
1 (bases 1 to 51)
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 5033 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source
1.51
/organism="Homo sapiens"
/db_xref="taxon:9606"
misc-feature
26
/note="1 of 2 allelic variants (5034 is other entry)
Accession number C943981141"
BASE COUNT 13 a 11 c 13 g 14 t
ORIGIN

Query Match 0.9%; Score 26; DB 6; Length 51;
Best Local Similarity 70.0%; Pred. No. 3.6e+04;
Matches 35; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1687 CATTTGTATGCTGCTGAGTGTGGACGAGCGCTTAAATGATAGCCACCCCTC 1736
51 CTTATGAATGTACAGAGTGTGGAGAGCCCTTCAACATAGTTCCACCCCTC 2

RESULT 12
AX382515
LOCUS AX382515 60 bp DNA linear PAT 18-MAR-2002
DEFINITION Sequence 45 from Patent WO0208286.
ACCESSION AX382515
VERSION AX382515.1 GI:19577266
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequences.

REFERENCE
1
AUTHORS Sera, T.
TITLE Zinc finger domain recognition code and uses thereof
JOURNAL Patent: WO 0208286-A 45 31-JAN-2002;
Syngenta Participations AG (CH)
FEATURES
source
1.60
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Partial zinc finger domain oligomer."
BASE COUNT 18 a 9 c 19 g 14 t
ORIGIN

Query Match 0.9%; Score 25.8; DB 6; Length 60;
Best Local Similarity 73.3%; Pred. No. 4.3e+04;
Matches 33; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1593 GGGGAGACCATTTATGTATGACGAGTGTGGCGAGGCTTACC 1637
1 GGGGAGAGACCGGTATTAATGTCGGAATGTGTAAAGATTGTTAGC 45

RESULT 13
AX382510
LOCUS AX382510 56 bp DNA linear PAT 18-MAR-2002
DEFINITION Sequence 40 from Patent WO0208286.
ACCESSION AX382510
VERSION AX382510.1 GI:19577261
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequences.

REFERENCE
1
AUTHORS Sera, T.
TITLE Zinc finger domain recognition code and uses thereof
JOURNAL Patent: WO 0208286-A 40 31-JAN-2002;
Syngenta Participations AG (CH)
FEATURES
Location/Qualifiers

Query Match 0.9%; Score 23.8; DB 6; Length 51;
Best Local Similarity 66.7%; Pred. No. 1.8e+05;
Matches 34; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 2475 CTTCCCATTTGGTGGCTTTCCCTCCGATTCACCAACCTTCACCTATT 2525
Db 51 CTCCTCGGGCGGTGGGCTCCCTCCGATTCCTTCACGCGATGACATATT 1

RESULT 18
AX382511/c 55 bp DNA linear PAT 18-MAR-2002
LOCUS Sequence 41 from Patent WO0208286.

DEFINITION AX382511
ACCESSION AX382511
VERSION AX382511.1 GI:19577262
KEYWORDS

SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 artificial sequences.

AUTHORS Sera,T.
TITLE Zinc finger domain recognition code and uses thereof
JOURNAL Patent: WO 0208286-A 41 31-JAN-2002;
SYNGENTA Participations AG (CH)
LOCATION/Qualifiers

FEATURES 1.55
source /organism="synthetic construct"
/db_xref="taxon:32630"

BASE COUNT 7 a 11 c 14 t 12 others
ORIGIN

Query Match 0.9%; Score 23.8; DB 6; Length 55;
Best Local Similarity 56.4%; Pred. No. 1.8e+05;
Matches 31; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1547 CTTAGCCTGAGTCAACCTTACAAACACGAGGTCAACGCGGAGAG 1601
Db 55 CTTAGTNNNAGTNNNNNTTACANNNCACCAACGACGACGCGGAGAG 1

RESULT 19
AX159659/c 51 bp DNA linear PAT 22-JUN-2001
LOCUS Sequence 2987 from Patent WO0140521.
DEFINITION AX159659
ACCESSION AX159659
VERSION AX159659.1 GI:14540990
KEYWORDS

SOURCE human.
ORGANISM Homo sapiens.
REFERENCE 1 Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
JOURNAL methods of use thereof
PATENT: WO 0140521-A 2987 07-JUN-2001;
CURAGEN CORPORATION (US)

FEATURES Location/Qualifiers
source 1.51
/organism="Homo sapiens"

BASE COUNT 21 a 9 c 12 g 9 t
ORIGIN /db_xref="taxon:9606"

misc_feature /note="1 of 2 allelic variants (2988 is other entry)
Accession number C942708452"

Query Match 0.8%; Score 23; DB 6; Length 51;
Best Local Similarity 74.4%; Pred. No. 3.1e+05;
Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2723 GAGAGCTGTCTTTTGGCTCAATAAATCTTTCTACCC 2761
Db 43 GAGCTTCTCTTTTGGCTTAACTTCACTTCGTTCACAC 5

RESULT 20
AX199545 51 bp DNA linear PAT 29-AUG-2001
LOCUS Sequence 475 from Patent WO0151670.

DEFINITION AX199545
ACCESSION AX199545
VERSION AX199545.1 GI:15389970
KEYWORDS

SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Shimkets,R.A. and Leach,M.D.
TITLE Nucleic acids containing single nucleotide, polymorphisms and
JOURNAL methods of use thereof
PATENT: WO 0151670-A 475 19-JUL-2001;
CURAGEN CORPORATION (US)

FEATURES Location/Qualifiers
source 1.51
/organism="Homo sapiens"

misc_feature /db_xref="taxon:9606"

BASE COUNT 13 a 16 c 14 g 8 t
ORIGIN

Query Match 0.8%; Score 23; DB 6; Length 51;
Best Local Similarity 68.1%; Pred. No. 3.1e+05;
Matches 32; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1056 TCAACCTGATTCACATCAGAGACACTCAGGAGGAACCTTA 1102
Db 4 TCGCATGTGAAGGCGCATCTGCGACGACACAGAGGTAGAAGCCCTA 50

RESULT 21
AX449256 60 bp DNA linear PAT 03-JUL-2002
LOCUS Sequence 34 from Patent WO0206327.
DEFINITION AX449256
ACCESSION AX449256
VERSION AX449256.1 GI:21698014
KEYWORDS

SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 Wang,Z. and Xiao,W.
A method for prognosing cancer and the proteins involved

JOURNAL Patent: WO 0206327-A 34 24-JAN-2002;
NORTHWESTERN UNIVERSITY (US)
LOCATION/Qualifiers

FEATURES 1.60
source /organism="synthetic construct"

BASE COUNT 11 a 16 c 17 g 16 t
ORIGIN /db_xref="taxon:32630"

Query Match 0.8%; Score 23; DB 6; Length 60;
Best Local Similarity 68.1%; Pred. No. 3.2e+05;
Matches 32; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 89 TCAGATCCGGCGGCGGTCCATCTGCTTCGAGACTT 135
Db 6 TCTGATCCGAGGTGAGTACTGACGCTTACACACGCTTCCGACCTT 52

[illegible]

BASE COUNT	12 a	9 c	15 g	12 t	12 others
ORIGIN					
Query Match	0.8%;	Score 22.4;	DB 6;	Length 60;	
Best Local Similarity	81.2%;	Pred. No. 4.9e+05;			
Matches	26;	Conservative	0;	Mismatches	6;
				Indels	0;
				Gaps	0;
Oy	1239	CACGAGAGGGCGACACATGCGGAGAAAGCCTTA	1270		
Db	36	CATCAGCGTACTACACATGCGGAGAAAGCCTTA	5		
RESULT 24					
AX382518/c					
LOCUS	AX382518		60 bp	DNA	Linear
DEFINITION	Sequence	48	from Patent	WO0208286.	PAT 18-MAR-2002
ACCESSION	AX382518				
VERSION	AX382518.1		GI:19577269		
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE	1				
AUTHORS	Sera,T				
TITLE	Zinc finger domain recognition code and uses thereof				
JOURNAL	Patent: WO 0208286-A 48 31-JAN-2002;				
SYNGENTA	Participations AG (CH)				
LOCATION/QUALIFIERS					
FEATURES	1..60				
SOURCE	/organism="synthetic construct"				
	/db_xref="taxon:32630"				
BASE COUNT	15 a	11 c	19 g	15 t	
ORIGIN					
Query Match	0.8%;	Score 22.4;	DB 6;	Length 60;	
Best Local Similarity	81.2%;	Pred. No. 4.9e+05;			
Matches	26;	Conservative	0;	Mismatches	6;
				Indels	0;
				Gaps	0;
Oy	1239	CACGAGAGGGCGACACATGCGGAGAAAGCCTTA	1270		
Db	36	CATCAGCGTACTACACATGCGGAGAAAGCCTTA	5		
RESULT 25					
AX163386/c					
LOCUS	AX163386		51 bp	DNA	Linear
DEFINITION	Sequence	6714	from Patent	WO0140521.	PAT 22-JUN-2001
ACCESSION	AX163386				
VERSION	AX163386.1		GI:14544717		
KEYWORDS					
SOURCE					
ORGANISM					
	human.				
	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1				
AUTHORS	Shimkets,R.A. and Leach,M.				
TITLE	Nucleic acids containing single nucleotide polymorphisms and				
	methods of use thereof				
JOURNAL	Patent: WO 0140521-A 6714 07-JUN-2001;				
CURAGEN	Corporation (US)				
LOCATION/QUALIFIERS					
FEATURES	1..51				
SOURCE	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
misc-feature	26				
	/note="2 of 2 allelic variants (6713 is other entry)				
BASE COUNT	15 a	12 c	17 g	7 t	
ORIGIN					
Query Match	0.8%;	Score 22.2;	DB 6;	Length 51;	

Best Local Similarity 64.7%; Pred. No. 5.5e+05;
Matches 33; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
OY 2475 CTTCCTGTTGGTGTCTTCCTCCGATGATCCCAACCTTCACCTATTT 2525
Db 51 CTCTCTGGGGGGGTGGCTCCCTCCATTTCTTCACGCGATGACATATTT 1

RESULT 26
AX115765/c 51 bp DNA linear PAT 11-MAY-2001
LOCUS AX115765
DEFINITION Sequence 888 from Patent WO0129262.
ACCESSION AX115765
VERSION AX115765.1 GI:14032707
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 51)
AUTHORS Picoult-Newburg, L. and Pohl, M.
TITLE Picoult-Newburg, L. and Pohl, M.
JOURNAL Patent: WO 0129262-A 888 26-APR-2001;
Ochid Biosciences, Inc. (US)
FEATURES
source Location/Qualifiers
1..51
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 11 a 9 c 14 g 17 t
ORIGIN

Query Match 0.8%; Score 21.8; DB 6; Length 51;
Best Local Similarity 70.7%; Pred. No. 7.3e+05;
Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
OY 1969 GCGAGTCACACCTCATTTAGACACCGAGAGACATTAGGA 2009
Db 42 GCCTGTGACACCTCATTTAGACACCTAGACACTTACCAAGA 2

RESULT 27
AR036764/c 41 bp DNA linear PAT 29-SEP-1999
LOCUS AR036764
DEFINITION Sequence 6 from patent US 5800984.
ACCESSION AR036764
VERSION AR036764.1 GI:5954620
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 41)
AUTHORS Vary, C.P.H.
TITLE Nucleic acid sequence detection by triple helix formation at primer
JOURNAL site in amplification reactions
FEATURES Patent: US 5800984-A 6 01-SEP-1998;
source Location/Qualifiers
1..41
/organism="unknown"
BASE COUNT 6 a 16 c 7 g 12 t
ORIGIN

Query Match 0.8%; Score 21.6; DB 6; Length 41;
Best Local Similarity 75.0%; Pred. No. 8.2e+05;
Matches 27; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
OY 374 GCGAGGGAGAGCGCCCTGAGAGAGAGAGAAAATG 409
Db 39 GCGTTCTGATCGCTTGAGAGAAAGAGAGAAAAG 4

RESULT 28
AF062523 60 bp DNA linear ROD 30-OCT-2001
LOCUS AF062523

DEFINITION Mus musculus antimicrobial mRNA sequence.
ACCESSION AF062523
VERSION AF062523.1 GI:16516872
KEYWORDS
SOURCE Mus musculus.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 60)
AUTHORS Ajidagba, P.A.
TITLE Direct Submission
JOURNAL Submitted (30-APR-1998) Veterinary Microbiology, Tuskegee
University, Carver Research Foundation Old Montgomery Road,
Tuskegee, AL 36088, USA
FEATURES
source Location/Qualifiers
1..60
/organism="Mus musculus"
/strain="C.D2 Vll-6"
/db_xref="taxon:10090"
/cell_type="macrophage"
/tissue_type="peritoneum"
/note="adherent peritoneal exudate cells; associated with
antimicrobial activity; similar to rearranged antigen
receptor"
BASE COUNT 21 a 11 c 19 g 9 t
ORIGIN

Query Match 0.8%; Score 21.6; DB 10; Length 60;
Best Local Similarity 63.5%; Pred. No. 8.6e+05;
Matches 33; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
OY 369 CTGGAGGAGGAGGAGCGCCCTGGAGAGAGAGAGAAAATGTCCTGAGACC 420
Db 1 CTGGAGGAGGAGGAGAGAGGTCGTGGCAATGAGAGAGAGAGAGAGAGAGAGAG 52

RESULT 29
AX159660/c 51 bp DNA linear PAT 22-JUN-2001
LOCUS AX159660
DEFINITION Sequence 2988 from patent WO0140521.
ACCESSION AX159660
VERSION AX159660.1 GI:14540991
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
JOURNAL methods of use thereof
FEATURES Patent: WO 0140521-A 2988 07-JUN-2001;
source Location/Qualifiers
1..51
/organism="Homo sapiens"
/db_xref="taxon:9606"
misc-feature
26
/note="2 of 2 allelic variants (2987 is other entry)
Accession number c942708452"
BASE COUNT 20 a 9 c 12 g 10 t
ORIGIN

Query Match 0.8%; Score 21.4; DB 6; Length 51;
Best Local Similarity 71.8%; Pred. No. 9.7e+05;
Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
OY 2723 GAGAGCTGTCTTGTGCAATAAATCTTCTTACCC 2761
Db 43 GAGCTTCTTCTTGTGCAATAAATCTTCTTCAACC 5

RESULT 30

LOCUS	AX449255	60 bp	DNA	linear	PAT 03-JUL-2002
DEFINITION	Sequence 33 from Patent WO0206327.				
ACCESSION	AX449255				
VERSION	AX449255.1	GI:21698013			
KEYWORDS					
SOURCE	synthetic construct.				
ORGANISM	artificial sequences.				
REFERENCE	1				
AUTHORS	Wang, Z. and Xiao, W.				
TITLE	A method for prognosing cancer and the proteins involved				
JOURNAL	Patent: WO 0206327-A 33 24-JAN-2002;				
	Northwestern University (US)				
FEATURES	location/Qualifiers				
source	1..60				
	/organism="synthetic construct"				
	/db_xref="taxon:32630"				
	/note="primer"				
BASE COUNT	11 a 16 c 16 g 17 t				
ORIGIN					
Query Match	0.8%; Score 21.4; DB 6;				
Best Local Similarity	66.0%; Pred. No. 9.9e+05;				
Matches	31; Conservative 0; Mismatches 16; Indels 0; Gaps 0;				
OY	89 TCAGATCCGGCGGTGCACCCGGCTTCATCTGTTCTGAGACTT 135				
Db	6 TCTGGATCCGAGGTGAGTACTGACTTTCACACGCTCTCCGAGCTT 52				
RESULT 31					
LOCUS	AX158732	50 bp	DNA	linear	PAT 22-JUN-2001
DEFINITION	Sequence 2060 from Patent WO0140521.				
ACCESSION	AX158732				
VERSION	AX158732.1	GI:14540063			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 50)				
AUTHORS	Shinkets, R.A. and Leach, M.				
TITLE	Nucleic acids containing single nucleotide polymorphisms and				
JOURNAL	methods of use thereof				
	Patent: WO 0140521-A 2060 07-JUN-2001;				
	Curagen Corporation (US).				
FEATURES	location/Qualifiers				
source	1..50				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
	25..26				
	/note="Nucleotide deleted between bases 25 and 26				
	Accession number cg38420254"				
BASE COUNT	15 a 14 c 12 g 9 t				
ORIGIN					
Query Match	0.8%; Score 21.2; DB 6;				
Best Local Similarity	69.0%; Pred. No. 1.1e+06;				
Matches	29; Conservative 0; Mismatches 13; Indels 0; Gaps 0;				
OY	2278 AAGAGAATTGCTGCTCATTTTCAGAGACCCCTGCCCTTCT 2319				
Db	8 AAGACAATGTCCTGCCAATAATCAGAGAGGCTCCACTTCT 49				
RESULT 32					
LOCUS	HSAD2S16/c	59 bp	DNA	linear	PRI 14-APR-1998
DEFINITION	Homo sapiens beta-adducin (ADD2) gene, exon 9, 5' partial sequence.				

[illegible]

LOCUS AX382526 45 bp DNA Linear PAT 18-MAR-2002
DEFINITION Sequence 56 from Patent WO0208286.
ACCESSION AX382526
VERSION AX382526.1 GI:19577277
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Sera,T.
TITLE Zinc finger domain recognition code and uses thereof
JOURNAL Patent: WO 0208286-A 56 31-JAN-2002;
Syngenta Participations AG (CH)
FEATURES
source 1.
45
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="PCR primer."
BASE COUNT 0 a 15 c 17 g 13 t
ORIGIN

Query Match 0.8%; Score 21; DB 6; Length 45;
Best Local Similarity 82.8%; Pred. No. 1.3e+06;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1239 CACCAGAGGGCGCAGCTGGGAGAGAACCC 1267
||||| | ||||| | ||||| | ||||| |
Db 45 CACCAACGCGACGACGAGGAGAGAACCC 17

RESULT 35
LOCUS AB4824 48 bp DNA Linear PAT 21-JAN-2000
DEFINITION Sequence 19 from Patent WO9844121.
ACCESSION AB4824
VERSION AB4824.1 GI:6733689
KEYWORDS
SOURCE Human adenovirus type 5.
ORGANISM Human adenovirus type 5
REFERENCE 1 (bases 1 to 48)
AUTHORS Mehtali,M. and Legrand,V.
TITLE MODIFIED ADENOVIRAL FIBER AND TARGET ADENOVIRUSES
JOURNAL Patent: WO 9844121-A 19 08-OCT-1998;
MEHTALI MAJID (FR); LEGRAND VALERIE (FR)
FEATURES
source 1.
48
/organism="Human adenovirus type 5"
/strain="ADENOVIRUS 5 (AD5)"
/isolate="OLIGONUCLEOTIDE DE SYNTHÈSE OTGD (REMPL. COUDE
SGTV EN DKU7)"
/db_xref="taxon:28285"
BASE COUNT 13 a 9 c 12 g 14 t
ORIGIN

Query Match 0.8%; Score 21; DB 6; Length 48;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 30; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 853 AATATGAAGTTTGGCCAGGCTTATCAAGAGTCAACCTCC 897
|| |||| | ||||| | || ||||| | || ||||| | || ||||| |
Db 4 AAGATGAGCACTTGGGTGCTATGTTGAGGCAACTGCC 48

RESULT 36
LOCUS ARI07677/c 50 bp DNA Linear PAT 14-FEB-2001
DEFINITION Sequence 30 from patent US 6110665.
ACCESSION ARI07677
VERSION ARI07677.1 GI:12823164
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 50)
TITLE Fenger,C.K., Granstrom,D.E., Gajadhar,A.A. and Dubey,J.P.
JOURNAL Sarcocystis neuradidagnostic primer and its use in methods of
equine protozoal myeloencephalitis diagnosis
Patent: US 6110665-A 30 29-AUG-2000;
FEATURES
source 1.
50
/organism="unknown"
BASE COUNT 2 a 8 c 19 g 12 t 9 others
ORIGIN

Query Match 0.8%; Score 21; DB 6; Length 50;
Best Local Similarity 58.7%; Pred. No. 1.3e+06;
Matches 27; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 1637 CCGGAATCAACCTGATCAAGCAGCAGAGACACTCAGGGAG 1682
||||| | ||||| | || ||||| | || ||||| | || ||||| |
Db 50 CCGGAACGAAACCTAATNCCCNNAACNNACNCCAGCGGAG 5

RESULT 37
LOCUS ARI68446/c 52 bp DNA Linear PAT 17-DEC-2001
DEFINITION Sequence 72 from patent US 6287854.
ACCESSION ARI68446
VERSION ARI68446.1 GI:17904368
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 52).
AUTHORS Spurr,N.K., Gray,I.C. and Stewart,L.M.
TITLE Diagnosis of susceptibility to cancer and treatment thereof
JOURNAL Patent: US 6287854-A 72 11-SEP-2001;
FEATURES
source 1.
52
/organism="unknown"
BASE COUNT 20 a 7 c 13 g 12 t
ORIGIN

Query Match 0.8%; Score 21; DB 6; Length 52;
Best Local Similarity 82.8%; Pred. No. 1.3e+06;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 528 CTGTTTCAGTTTATGCGAGGAATCC 556
||||| | ||||| | || ||||| | || ||||| | || ||||| |
Db 41 CTGTTTCAGTTTCTCGAGGAATCC 13

RESULT 38
LOCUS ARI65671 59 bp DNA Linear PAT 17-OCT-2001
DEFINITION Sequence 236 from patent US 6280932.
ACCESSION ARI65671
VERSION ARI65671.1 GI:16240652
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 59)
AUTHORS Parma,D.H., Hicke,B., Bridonneau,P. and Gold,L.
TITLE High affinity nucleic acid ligands to lectins
JOURNAL Patent: US 6280932-A 236 28-AUG-2001;
FEATURES
source 1.
59
/organism="unknown"
BASE COUNT 22 a 16 c 15 g 6 t
ORIGIN

Query Match 0.8%; Score 21; DB 6; Length 59;
Best Local Similarity 66.7%; Pred. No. 1.3e+06;
Matches 30; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

PUBMED 8297127
 FEATURES
 source Location/Qualifiers
 1..60 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /map="17q22"
 misc_feature 1..60
 BASE COUNT 7 a 14 c 11 g 28 t
 ORIGIN

Query Match 0.7%: Score 20.6; DB 9: Length 60;
 Best Local Similarity 59.3%: Pred. No. 1.8e+06;
 Matches 35: Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1980 CTCATTAGACACACAGACATTCAGAGAGAGCCTTATTTTCAGAACTGTG 2033
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 Db 60 CTCACAGACAGAGAGATGTGTCAAGAGAGAAACATTCACAGCAGAAATGTGG 2

RESULT 48
 AX158272 51 bp DNA linear PAT 22-JUN-2001
 LOCUS AX158272/c
 DEFINITION Sequence 1600 from Patent WO0140521.
 ACCESSION AX158272
 VERSION AX158272.1 GI:14539603
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 (bases 1 to 51)
 AUTHORS Shimkets,R.A. and Leach,M.
 TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
 JOURNAL Patent: WO 0140521-A 1600 07-JUN-2001;
 FEATURES
 source Location/Qualifiers
 1..51 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 misc_feature 26
 /note="2 of 2 allelic variants (1599 is other entry)
 Accession number c93079374"
 BASE COUNT 10 a 14 c 14 g 13 t
 ORIGIN

Query Match 0.7%: Score 20.4; DB 6: Length 51;
 Best Local Similarity 65.2%: Pred. No. 2e+06;
 Matches 30: Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 752 CACAGTGTGATATAGTTCAGACCTGAACGAGGAGGAGATCTA 797
 111111 111111 111111 111111 111111 111111 111111 111111
 Db 48 CCCAGTGTGATATAGTTCAGACCTGAACGAGGAGGAGATCTCA 3

RESULT 49
 D50270 52 bp DNA linear ROD 14-APR-2000
 LOCUS D50270/c
 DEFINITION Mouse Pig-f DNA, exon 3 5'-boundary sequence.
 ACCESSION D50270
 VERSION D50270.1 GI:1753184
 KEYWORDS
 SOURCE Pig-f.
 ORGANISM Mus musculus DNA.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (sites)
 AUTHORS Ohishi,K., Kurimoto,Y., Inoue,N., Endo,Y., Takeda,J. and
 Kinoshita,T.
 TITLE Cloning and characterization of the murine GPI anchor synthesis
 gene Pigf, a homologue of the human PI6F gene
 JOURNAL Genomics 34 (3), 340-346 (1996)
 MEDLINE 96374826

REFERENCE 2 (bases 1 to 52)
 AUTHORS Ohishi,K.
 TITLE Cloning and characterization of the GPI-anchor synthesis gene
 JOURNAL Pig-f murine homologue to human PI6-F gene
 REFERENCE 3 (bases 1 to 52)
 AUTHORS Ohishi,K.
 TITLE Direct Submission
 JOURNAL Submitted (12-APR-1995) Kazuhiro Ohishi, Research Institute for
 Microbial Diseases, Osaka University, Immunoregulation; 3-1
 Yamada-oka, Suita, Osaka 565, Japan (tel:06-875-5233,
 fax:06-875-5233)
 Location/Qualifiers
 1..52 /organism="Mus musculus"
 /db_xref="taxon:10090"
 1..52 /gene="Pig-f"
 <1..42 /gene="Pig-f"
 /note="mouse Pig-f exon3 5'-boundary"
 43..52 /number=2
 /gene="Pig-f"
 /number=3
 BASE COUNT 11 a 11 c 10 g 20 t
 ORIGIN

Query Match 0.7%: Score 20.4; DB 10: Length 52;
 Best Local Similarity 65.2%: Pred. No. 2e+06;
 Matches 30: Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1457 GCGTCACCTTACGTCGAATCAACCTCAACACACACAGAGACA 1502
 111111 111111 111111 111111 111111 111111 111111 111111
 Db 49 GCGTTACCTAAGACAGAAATGAGATTTCTGAGACTCTCAGAGATA 4

RESULT 50
 AR040811/c 50 bp DNA linear PAT 29-SEP-1999
 LOCUS AR040811
 DEFINITION Sequence 40 from patent US 5811231.
 ACCESSION AR040811
 VERSION AR040811.1 GI:5961307
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 50)
 AUTHORS Fair,S.B. and Todd,M.D.
 TITLE Methods and kits for eukaryotic gene profiling
 JOURNAL Patent: US 5811231-A 40 22-SEP-1998;
 FEATURES
 source Location/Qualifiers
 1..50 /organism="unknown"
 BASE COUNT 15 a 16 c 8 g 11 t
 ORIGIN

Query Match 0.7%: Score 20.2; DB 6: Length 50;
 Best Local Similarity 68.3%: Pred. No. 2.3e+06;
 Matches 28: Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2212 TCGACACATTCGTGTGATATGATGATGAGACTGTACTGG 2252
 111111 111111 111111 111111 111111 111111 111111 111111
 Db 48 TGCACACATTCAGTGTCTACCGTTGAAGAGAGAGTGGAGTGG 8

Search completed: June 4, 2003, 09:16:59
 Job time : 7203 secs